

From: Chan, Christina
Sent: Tuesday, May 03, 2005 5:27 PM
To: Holleran, Anne; STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search for 09/977,406

Please ~~rush~~. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
MAY -4 2005
(STIC)

-----Original Message-----

From: Holleran, Anne
Sent: Tuesday, May 03, 2005 5:04 PM
To: Chan, Christina
Subject: RUSH sequence search for 09/977,406

Please approve and forward to STIC the following RUSH sequence search request. This is for an amendment due this biweek. Thanks.

Please search the following sequences for 09/977,406:

oligomer search of SEQ ID NO: 5 (aa) (commercial and interference)
SEQ ID NO: 58 (aa) (commercial and interference)
SEQ ID NO: 59 (aa) (commercial and interference)
SEQ ID NO: 88(aa) (commercial and interference)
SEQ ID NO: 90 (aa) (commercial and interference)
SEQ ID NO: 91 (aa) (commercial and interference)
SEQ ID NO: 92 (aa) (commercial and interference)

These sequences are all related by including all or parts of SEQ ID NO: 5.

Anne Holleran
AU: 1642
Tel: (571) 272-0833
RM: Remsen, 3A14

mailbox: Remsen, 3C18

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:03:32 ; Search time 30.3273 Seconds
(without alignments)
191.293 Million cell updates/sec

Title: US-09-977-406a-5

Perfect score: 15

Sequence: 1 EMQDNCCTCTCYET 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	AAO17915	AAO17915 Human pro
2	15	100.0	15	ABR56231	ABR56231 Prostate
3	15	100.0	16	AAO17917	AAO17917 Human pro
4	15	100.0	16	AAO17966	AAO17966 Human pro
5	15	100.0	17	AAO17967	AAO17967 Human pro
6	15	100.0	17	AAO17918	AAO17918 Human pro
7	15	100.0	18	AAO17919	AAO17919 Human pro
8	15	100.0	18	AAO17968	AAO17968 Human pro
9	15	100.0	19	AAO17969	AAO17969 Human pro
10	15	100.0	19	AAO17920	AAO17920 Human pro
11	15	100.0	20	AAO17921	AAO17921 Human pro
12	15	100.0	20	AAO17970	AAO17970 Human pro
13	15	100.0	21	AAO17922	AAO17922 Human pro
14	15	100.0	21	AAO17971	AAO17971 Human pro
15	15	100.0	22	AAO17923	AAO17923 Human pro
16	15	100.0	22	AAO17972	AAO17972 Human pro
17	15	100.0	23	AAO17973	AAO17973 Human pro
18	15	100.0	23	AAO17924	AAO17924 Human pro
19	15	100.0	24	AAO17925	AAO17925 Human pro
20	15	100.0	24	AAO17974	AAO17974 Human pro
21	15	100.0	25	AAO17975	AAO17975 Human pro
22	15	100.0	25	AAO17926	AAO17926 Human pro
23	15	100.0	26	AAO17976	AAO17976 Human pro
24	15	100.0	26	AAO17927	AAO17927 Human pro
25	15	100.0	27	AAO17977	AAO17977 Human pro

ALIGNMENTS

26	15	100.0	27	5	AAO17928	AAO17928 Human pro
27	15	100.0	28	5	AAO17929	AAO17929 Human pro
28	15	100.0	28	5	AAO17978	AAO17978 Human pro
29	15	100.0	29	5	AAO17930	AAO17930 Human pro
30	15	100.0	29	5	AAO17979	AAO17979 Human pro
31	15	100.0	30	5	AAO17980	AAO17980 Human pro
32	15	100.0	30	5	AAO17997	AAO17997 Human pro
33	15	100.0	30	5	AAO17931	AAO17931 Human pro
34	15	100.0	31	5	AAO17981	AAO17981 Human pro
35	15	100.0	31	5	AAO17932	AAO17932 Human pro
36	15	100.0	32	5	AAO17933	AAO17933 Human pro
37	15	100.0	32	5	AAO17982	AAO17982 Human pro
38	15	100.0	33	5	AAO17934	AAO17934 Human pro
39	15	100.0	33	5	AAO17983	AAO17983 Human pro
40	15	100.0	34	5	AAO17935	AAO17935 Human pro
41	15	100.0	34	5	AAO17984	AAO17984 Human pro
42	15	100.0	35	5	AAO17936	AAO17936 Human pro
43	15	100.0	35	5	AAO17985	AAO17985 Human pro
44	15	100.0	36	5	AAO17937	AAO17937 Human pro
45	15	100.0	36	5	AAO17986	AAO17986 Human pro

RESULT 1
AAO17915
ID AAO17915 standard; peptide; 15 AA.
XX AAO17915;
AC
XX
DT 30-AUG-2002 (first entry)
XX
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #4.
XX
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
XX
OS Homo sapiens.
XX
XX
PN W0200233090-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02322256.
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROCYN) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
DR New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX
PS Claim 1; Page 74; 185pp; English.
XX
XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention

XX Sequence 15 AA;

Query Match 100.0%; Score 15; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQDNCETCTCYET 15
1 EMQDNCETCTCYET 15

RESULT 2
ID ABR56231 standard; peptide; 15 AA.
ABR56231

AC ABR56231;
DT 20-NOV-2003 (first entry)

DE Prostate secretory protein-94 (PSP-94) peptide fragment PCK3145.

KW Cytostatic; prostate secretory protein-94; PSP-94; human;
hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;
parathyroid hormone related peptide; PTHrP; skeletal metastasis.

OS Homo sapiens.

PN W02003039576-A1.

PD 15-MAY-2003.

PF 08-NOV-2002; 2002WO-CA001737.

PR 08-NOV-2001; 2001CA-02361736.

PS (PROC-) PROCYON BIOPHARMA INC.

PI Rabbani SA, Shukelir N, Panchal CJ, Newman C;

WPI; 2003-441476/41.

PT Use of prostate secretory protein-94 for treating hypercalcaemia of
malignancy and reducing skeletal metastasis arising from carcinomas,
prostate and breast cancers.

PS Disclosure; Page 37; 61pp; English.

CC The present invention relates to the use of prostate secretory protein-94
(PSP-94; ABR56227-ABR56228) for treating a patient suffering from
hypercalcaemia of malignancy. PSP-94 is useful for treating a patient
suffering from hypercalcaemia of malignancy arising from carcinomas,
prostate and breast cancer. The PSP-94 is also useful for reducing
parathyroid hormone related peptide (PTHrP) levels in a patient in need
and reducing the development of skeletal metastasis. The PSP-94 is also
used for the manufacture of a pharmaceutical composition for the
treatment of hypercalcaemia of malignancy and/or skeletal metastasis. The
present sequence is a peptide fragment of PSP-94, used to illustrate the
invention

CC Sequence 15 AA;

Query Match 100.0%; Score 15; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQDNCETCTCYET 15
1 EMQDNCETCTCYET 15

RESULT 3
AA017917

ID AA017917 standard; peptide; 16 AA.

AC AA017917;

DT 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #6.

KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
beta-microseminoprotein; human seminal plasma inhibin; analogue;
prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
benign prostate hyperplasia; cyostatic.

OS Homo sapiens.

PN W0200233090-A2.

PD 25-APR-2002.

PF 15-OCT-2001; 2001WO-CA001463.

PR 16-OCT-2000; 2000CA-02321256.

PR 20-AUG-2001; 2001CA-02355334.

PS (PROC-) PROCYON BIOPHARMA INC.

PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

PT New human prostate secretory protein of 94 amino acids, useful for
inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
gastrointestinal, breast, endometrial, and ovarian cancers.

PS Claim 2; Page 76; 185pp; English.

CC The present invention relates to analogues of the human prostate
secretory protein of 94 amino acids (PSP94, also known as prostatic
inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal
cancer, breast cancer, endometrial, ovarian or other cancers of
epithelial secretion, or benign prostate hyperplasia and for treating
patients with a disease characterized by elevated levels of FSH. The
present sequence is an analogue of the invention

CC Sequence 16 AA;

Query Match 100.0%; Score 15; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQDNCETCTCYET 15
1 EMQDNCETCTCYET 15

RESULT 4
ID AA017966 standard; peptide; 16 AA.
AA017966

AC AA017966;

DT 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #55.

KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
beta-microseminoprotein; human seminal plasma inhibin; analogue;
prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
benign prostate hyperplasia; cyostatic.

XX OS Homo sapiens.
 XX PI WO200233090-A2.
 XX PN 25-APR-2002.
 XX PD 15-OCT-2001; 2001WO-CA001463.
 XX PF 16-OCT-2000; 2000CA-02321256.
 XX PR 20-AUG-2001; 2001CA-02355334.
 XX PA (PROC-) PROCYON BIOPHARMA INC.
 XX PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX DR WPI; 2002-471401/50.
 XX PT New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX PS Claim 2; Page 94; 185pp; English.
 XX CC The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX SQ Sequence 16 AA;
 XX
 XX Query Match 100.0%; Score 15; DB 5; Length 16;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-10;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 EWQTDNCETCTCYET 15
 XX ||||||||||||
 XX Db 2 EWQTDNCETCTCYET 16
 XX
 XX RESULT 5
 XX AAO17967 standard; peptide; 17 AA.
 XX ID AAO17967;
 XX AC AAO17967;
 XX DT 30-AUG-2002 (first entry)
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #56.
 XX XX
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cyostatic.
 XX PA (PROC-) PROCYON BIOPHARMA INC.
 XX OS Homo sapiens.
 XX PI WO200233090-A2.
 XX PN 25-APR-2002.
 XX PD 15-OCT-2001; 2001WO-CA001463.
 XX PF 16-OCT-2000; 2000CA-02321256.
 XX PR 20-AUG-2001; 2001CA-02355334.
 XX PA (PROC-) PROCYON BIOPHARMA INC.

XX XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX DR WPI; 2002-471401/50.
 XX PT New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX PS Claim 2; Page 94; 185pp; English.
 XX CC The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX SQ Sequence 17 AA;
 XX
 XX Query Match 100.0%; Score 15; DB 5; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 EWQTDNCETCTCYET 15
 XX ||||||||||||
 XX Db 3 EWQTDNCETCTCYET 17
 XX
 XX RESULT 6
 XX AAO17918 standard; peptide; 17 AA.
 XX ID AAO17918;
 XX AC AAO17918;
 XX DT 30-AUG-2002 (first entry)
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #7.
 XX XX
 XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cyostatic.
 XX PA (PROC-) PROCYON BIOPHARMA INC.
 XX OS Homo sapiens.
 XX PI WO200233090-A2.
 XX PN 25-APR-2002.
 XX PD 15-OCT-2001; 2001WO-CA001463.
 XX PF 16-OCT-2000; 2000CA-02321256.
 XX PR 20-AUG-2001; 2001CA-02355334.
 XX PA (PROC-) PROCYON BIOPHARMA INC.
 XX OS Homo sapiens.
 XX PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX DR WPI; 2002-471401/50.
 XX PT New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX PS Claim 2; Page 76; 185pp; English.
 XX CC The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic

CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-microseminoprotein (bets-MSP). The analogues are useful for inhibiting growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal cancer, breast cancer, endometrial, ovarian or other cancers of epithelial secretion, or benign prostate hyperplasia and for treating patients with a disease characterized by elevated levels of FSH. The present sequence is an analogue of the invention

XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 15; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
| | | | | | | | | | | | | | | | |
Db 1 EMQDNCETCTCYET 15

RESULT 7
AAOI7919 standard; peptide; 18 AA.

XX AAOI7919;
AC
XX 30-AUG-2002 (first entry)
XX

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #8.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.

XX Homo sapiens.
XX WO200233090-A2.
XX

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 77; 185pp; English.

XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention

XX Sequence 18 AA;

Query Match 100.0%; Score 15; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
| | | | | | | | | | | | | | | | |
Db 1 EMQDNCETCTCYET 15

RESULT 8
AAOI7968 standard; peptide; 18 AA.

XX AAOI7968;
AC
XX 30-AUG-2002 (first entry)
XX

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #57.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.

XX Homo sapiens.
XX WO200233090-A2.
XX

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX

XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 94; 185pp; English.

XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention

XX Sequence 18 AA;

Query Match 100.0%; Score 15; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
| | | | | | | | | | | | | | | | |
Db 4 EMQDNCETCTCYET 18

RESULT 9
AAOI7969 standard; peptide; 19 AA.

XX AAOI7969;
AC
XX 30-AUG-2002 (first entry)
XX

XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #58.
XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP, HSPI, beta-MSP,
XX KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX KW benign prostate hyperplasia; cytostatic.
XX OS Homo sapiens.
XX PN WO200233090-A2.
XX PD 25-APR-2002.
XX PF 15-OCT-2001; 2001WO-CA001463.
XX PR 16-OCT-2000; 2000CA-02321256.
XX PR 20-AUG-2001; 2001CA-02355334.
XX PA (PROC-) PROCYON BIOPHARMA INC.
XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX DR WPI; 2002-471401/50.
XX PT New human prostate secretory protein of 94 amino acids, useful for
XX PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX PS Claim 2; Page 95; 185pp; English.
XX SQ
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 15; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e-10; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
OY 1 EMQDNCETCTCYET 15
Db |||||
5 EMQDNCETCTCYET 19
RESULT 10
ID AA017920 standard; peptide; 19 AA.
XX AA017920;
XX AC 30-AUG-2002 (first entry)
XX DT
XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #9.
XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP, HSPI, beta-MSP,
XX KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX KW benign prostate hyperplasia; cytostatic.
XX OS Homo sapiens.
XX PN WO200233090-A2.
XX DR WPI; 2002-471401/50.
XX

PD 25-APR-2002.
XX KW 15-OCT-2001; 2001WO-CA001463.
XX PR 16-OCT-2000; 2000CA-02321256.
XX PR 20-AUG-2001; 2001CA-02355334.
XX PA (PROC-) PROCYON BIOPHARMA INC.
XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX DR WPI; 2002-471401/50.
XX PT New human prostate secretory protein of 94 amino acids, useful for
XX PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX PS Claim 2; Page 77; 185pp; English.
XX SQ
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 15; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e-10; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;
OY 1 EMQDNCETCTCYET 15
Db |||||
1 EMQDNCETCTCYET 15
RESULT 11
ID AA017921 standard; peptide; 20 AA.
XX AA017921;
XX AC 30-AUG-2002 (first entry)
XX DT
XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #10.
XX KW Cancer; human; PSP94; prostatic inhibin protein; PIP, HSPI, beta-MSP,
XX KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX KW benign prostate hyperplasia; cytostatic.
XX OS Homo sapiens.
XX PN WO200233090-A2.
XX PD 25-APR-2002.
XX PF 15-OCT-2001; 2001WO-CA001463.
XX PR 16-OCT-2000; 2000CA-02321256.
XX PR 20-AUG-2001; 2001CA-02355334.
XX PA (PROC-) PROCYON BIOPHARMA INC.
XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX DR WPI; 2002-471401/50.
XX

PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
PS Claim 2; Page 77; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemioprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 20 AA;
XX
Query Match 100.0%; Score 15; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EWQTDNCETCTCYET 15
DB 1 EWQTDNCETCTCYET 15
XX
RESULT 12
AAOI7970
ID AAOI7970 standard; peptide; 20 AA.
XX
AC AAOI7970;
XX
XX 30-AUG-2002 (first entry)
DT
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #59.
DE
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
KW beta-microsemioprotein; human seminal plasma inhibin; analogue;
KW prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostatic hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200233090-A2.
PN
XX 25-APR-2002.
PD
XX 15-OCT-2001; 2001WO-CA001463.
PF
XX 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
PI WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 95; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemioprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating

CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 20 AA;
XX
Query Match 100.0%; Score 15; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EWQTDNCETCTCYET 15
DB 6 EWQTDNCETCTCYET 20
XX
RESULT 13
AAOI7922
ID AAOI7922 standard; peptide; 21 AA.
XX
AC AAOI7922;
XX
XX 30-AUG-2002 (first entry)
DT
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #11.
DE
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
KW beta-microsemioprotein; human seminal plasma inhibin; analogue;
KW prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostatic hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200233090-A2.
PN
XX 25-APR-2002.
PD
XX 15-OCT-2001; 2001WO-CA001463.
PF
XX 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
PI WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 78; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemioprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 21 AA;
XX
Query Match 100.0%; Score 15; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EWQTDNCETCTCYET 15
DB 1 EWQTDNCETCTCYET 15
XX

RESULT 14

AAO17971 standard; peptide; 21 AA.

AAO17971;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94 analogue #60.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-microseminoprotein; human seminal plasma inhibin; analogue;

Prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

benign prostate hyperplasia; cytostatic.

Homo sapiens.

MO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001MO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 95; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 21 AA;

Query Match 100.0%; Score 15; DB 5; Length 21;

Best Local Similarity 100.0%; Pred. No. 3.1e-10;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EMQTDNCETCTCYET 15

7 EMQTDNCETCTCYET 21

Db

RESULT 15

AAO17923 standard; peptide; 22 AA.

AAO17923;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94 analogue #12.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-microseminoprotein; human seminal plasma inhibin; analogue;

prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

benign prostate hyperplasia; cytostatic.

Homo sapiens.

MO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001MO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 78; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 22 AA;

Query Match 100.0%; Score 15; DB 5; Length 22;

Best Local Similarity 100.0%; Pred. No. 3.2e-10;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EMQTDNCETCTCYET 15

1 EMQTDNCETCTCYET 15

Db

Search completed: May 4, 2005, 14:25:09

Job time : 31.3273 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:13:33 ; Search time 7.69091 Seconds
(without alignments)
145.592 Million cell updates/sec

Title: US-09-977-406A-5

Perfect score: 15

Sequence: 1 EMQDNCCTCYET 15

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/6D_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	94	1 US-07-899-535A-1	Sequence 1, Appli
2	15	100.0	114	4 US-09-513-999C-7807	Sequence 7807, Ap
3	6	40.0	241	2 US-08-460-309-17	Sequence 17, Appl
4	6	40.0	241	2 US-08-125-077-17	Sequence 17, Appl
5	6	40.0	2123	4 US-09-949-016-7517	Sequence 7, Appli
6	6	40.0	3070	4 US-09-961-403-7	Sequence 7, Appli
7	6	40.0	3088	4 US-09-562-702A-8	Sequence 8, Appli
8	6	40.0	3089	4 US-09-562-702A-4	Sequence 8, Appli
9	6	40.0	3110	4 US-09-562-702A-2	Sequence 2, Appli
10	6	40.0	3110	4 US-09-562-702A-6	Sequence 6, Appli
11	6	40.0	3110	4 US-09-561-709B-7	Sequence 7, Appli
12	6	40.0	3110	4 US-09-917-254-86	Sequence 86, Appl
13	6	40.0	3110	4 US-09-949-016-5937	Sequence 5937, Ap
14	6	40.0	3111	2 US-08-460-309-4	Sequence 4, Appli
15	6	40.0	3111	2 US-08-125-077-4	Sequence 4, Appli
16	5	33.3	9	3 US-08-481-968A-24	Sequence 24, Appli
17	5	33.3	9	3 US-08-154-712B-24	Sequence 24, Appli
18	5	33.3	9	3 US-09-947-925A-24	Sequence 24, Appli
19	5	33.3	37	4 US-09-917-340-57	Sequence 57, Appli
20	5	33.3	37	4 US-09-829-481-11	Sequence 11, Appli
21	5	33.3	38	4 US-09-030-619-199	Sequence 199, App
22	5	33.3	38	4 US-09-030-619-200	Sequence 200, App
23	5	33.3	58	4 US-09-621-976-5440	Sequence 5440, Ap
24	5	33.3	104	4 US-09-621-976-6750	Sequence 6750, Ap
25	5	33.3	107	4 US-09-513-999C-7986	Sequence 7986, Ap
26	5	33.3	110	4 US-09-513-999C-7055	Sequence 7055, Ap
27	5	33.3	188	4 US-09-270-767-61692	Sequence 61692, A

28	5	33.3	230	4 US-09-248-796A-21826	Sequence 21826, A
29	5	33.3	231	4 US-09-265-540E-4	Sequence 4, Appli
30	5	33.3	243	2 US-08-460-309-15	Sequence 15, Appli
31	5	33.3	243	2 US-08-460-309-16	Sequence 16, Appli
32	5	33.3	243	2 US-08-125-077-15	Sequence 15, Appli
33	5	33.3	243	2 US-08-125-077-16	Sequence 16, Appli
34	5	33.3	261	4 US-09-962-357-8	Sequence 8, Appli
35	5	33.3	315	4 US-09-902-540-14527	Sequence 14527, A
36	5	33.3	316	4 US-09-543-681A-5873	Sequence 5873, Ap
37	5	33.3	362	4 US-09-248-796A-20514	Sequence 20514, A
38	5	33.3	392	4 US-09-424-978B-39	Sequence 39, Appli
39	5	33.3	396	4 US-09-424-978B-36	Sequence 36, Appli
40	5	33.3	400	4 US-09-270-767-46136	Sequence 46136, A
41	5	33.3	454	4 US-09-134-000C-5977	Sequence 5977, Ap
42	5	33.3	689	4 US-09-937-215-2	Sequence 2, Appli
43	5	33.3	716	2 US-08-484-993B-14	Sequence 14, Appli
44	5	33.3	716	2 US-08-484-158B-14	Sequence 14, Appli
45	5	33.3	716	2 US-08-484-596A-14	Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-07-899-535A-1
Sequence 1, Application US/07899535A

Patent No. 5428011

GENERAL INFORMATION:

APPLICANT: Sheth, Anil R.

APPLICANT: Panchaj, Seema

TITLE OF INVENTION: Pharmaceutical Preparations For

TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate

TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mr. George Loud

STREET: 2001 Jefferson Davis Highway, Suite 306

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/899,535A

FILING DATE: 16-JUN-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Loud, George A.

REGISTRATION NUMBER: 25,814

REFERENCE/DOCKET NUMBER: S&B-A835

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-0960

TELEFAX: 703-415-0962

TELEX: 24 8614

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 94 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHEICAL: NO

US-07-899-535A-1

Query Match 100.0%; Score 15; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCYET 15
Db 31 EMQDNCCTCYET 45

RESULT 2

US-09-513-999C-7807
; Sequence 7807, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 7807
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; OTHER INFORMATION: score 9
US-09-513-999C-7807

Query Match 100.0%; Score 15; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCYET 15
Db 51 EMQDNCCTCYET 65

RESULT 3

US-08-460-309-17
; Sequence 17, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-17

Query Match 40.0%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCCTCT 11
Db 103 NCCTCT 108

RESULT 4

US-08-125-077-17
; Sequence 17, Application US/08125077
; Patent No. 5872231
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-17

Query Match 40.0%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 103 NCERTCT 108

RESULT 5
US-09-949-016-7517
Sequence 7517, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7517
LENGTH: 2123
TYPE: PRT
ORGANISM: Human
US-09-949-016-7517

Query Match 40.0%; Score 6; DB 4; Length 2123;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 405 NCERTCT 410

RESULT 6
US-09-961-403-7
Sequence 7, Application US/09961403
Patent No. 6780594
GENERAL INFORMATION:
APPLICANT: HE-STUWEP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTT, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 3070
TYPE: PRT
ORGANISM: Homo sapiens
US-09-961-403-7

Query Match 40.0%; Score 6; DB 4; Length 3070;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 7
US-09-562-702A-8
Sequence 8, Application US/09562702A
Patent No. 6632790
GENERAL INFORMATION:
APPLICANT: Yurchenco, Peter
TITLE OF INVENTION: Laminin 2 and Methods for Its Use
FILE REFERENCE: 99-274-B
CURRENT APPLICATION NUMBER: US/09/562,702A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/155,945
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 60/143,289
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/139,198
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/131,720
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 3088
TYPE: PRT
ORGANISM: Homo sapiens
US-09-562-702A-8

Query Match 40.0%; Score 6; DB 4; Length 3088;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 367 NCERTCT 372

RESULT 8
US-09-562-702A-4
Sequence 4, Application US/09562702A
Patent No. 6632790
GENERAL INFORMATION:
APPLICANT: Yurchenco, Peter
TITLE OF INVENTION: Laminin 2 and Methods for Its Use
FILE REFERENCE: 99-274-B
CURRENT APPLICATION NUMBER: US/09/562,702A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/155,945
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 60/143,289
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/139,198
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/131,720
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 3089
TYPE: PRT
ORGANISM: Homo sapiens
US-09-562-702A-4

Query Match 40.0%; Score 6; DB 4; Length 3089;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
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Db 367 NCERTCT 372

RESULT 9
US-09-562-702A-2
; Sequence 2, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-2

Query Match 40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
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Db 389 NCERTCT 394

RESULT 10
US-09-562-702A-6
; Sequence 6, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-6

Query Match 40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
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Db 389 NCERTCT 394

RESULT 11
US-09-561-709B-7
; Sequence 7, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeon, Robert
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-7

Query Match 40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
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Db 389 NCERTCT 394

RESULT 12
US-09-917-254-86
; Sequence 86, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Multer, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224 (JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentln Version 3.0
; SEQ ID NO 86
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-917-254-86

Query Match 40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
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Db 389 NCERTCT 394

RESULT 13
US-09-949-016-5937
; Sequence 5937, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 5937
LENGTH: 3110
TYPE: PRT
ORGANISM: Human
US-09-949-016-5937

Query Match 40.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 14
US-08-460-309-4
Sequence 4, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-4

Query Match 40.0%; Score 6; DB 2; Length 3111;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 15
US-08-125-077-4
Sequence 4, Application US/08125077
Patent No. 5872231
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3111 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-4

Query Match 40.0%; Score 6; DB 2; Length 3111;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NCERTCT 11
Db 389 NCERTCT 394

Thu May 5 15:11:08 2005

us-09-977-406a-5.oligo.ra1

Page 6

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Job time : 8.69091 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:33:36 ; Search time 16.7455 Seconds
(without alignments)
298.385 Million cell updates/sec

Title: US-09-977-406a-5
Perfect score: 15
Sequence: 1 EMQDNCETCTCYET 15

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Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Published Applications AA:*
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19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	15	100.0	15	17	US-10-291-360-5
3	15	100.0	15	17	US-10-857-358-5
4	15	100.0	16	10	US-09-977-406a-10
5	15	100.0	16	10	US-09-977-406a-59
6	15	100.0	17	10	US-09-977-406a-11
7	15	100.0	17	10	US-09-977-406a-60
8	15	100.0	18	10	US-09-977-406a-12
9	15	100.0	18	10	US-09-977-406a-61
10	15	100.0	19	10	US-09-977-406a-13
11	15	100.0	19	10	US-09-977-406a-62
12	15	100.0	20	10	US-09-977-406a-14
13	15	100.0	20	10	US-09-977-406a-63

14	15	100.0	21	10	US-09-977-406a-15	Sequence 15, Appl
15	15	100.0	21	10	US-09-977-406a-64	Sequence 64, Appl
16	15	100.0	22	10	US-09-977-406a-16	Sequence 16, Appl
17	15	100.0	22	10	US-09-977-406a-65	Sequence 65, Appl
18	15	100.0	23	10	US-09-977-406a-17	Sequence 17, Appl
19	15	100.0	23	10	US-09-977-406a-66	Sequence 66, Appl
20	15	100.0	24	10	US-09-977-406a-18	Sequence 18, Appl
21	15	100.0	24	10	US-09-977-406a-67	Sequence 67, Appl
22	15	100.0	25	10	US-09-977-406a-19	Sequence 19, Appl
23	15	100.0	25	10	US-09-977-406a-68	Sequence 68, Appl
24	15	100.0	26	10	US-09-977-406a-20	Sequence 20, Appl
25	15	100.0	26	10	US-09-977-406a-69	Sequence 69, Appl
26	15	100.0	27	10	US-09-977-406a-21	Sequence 21, Appl
27	15	100.0	27	10	US-09-977-406a-70	Sequence 22, Appl
28	15	100.0	28	10	US-09-977-406a-22	Sequence 23, Appl
29	15	100.0	28	10	US-09-977-406a-71	Sequence 24, Appl
30	15	100.0	29	10	US-09-977-406a-23	Sequence 25, Appl
31	15	100.0	29	10	US-09-977-406a-72	Sequence 26, Appl
32	15	100.0	30	10	US-09-977-406a-24	Sequence 27, Appl
33	15	100.0	30	10	US-09-977-406a-73	Sequence 28, Appl
34	15	100.0	30	10	US-09-977-406a-90	Sequence 29, Appl
35	15	100.0	31	10	US-09-977-406a-25	Sequence 30, Appl
36	15	100.0	31	10	US-09-977-406a-74	Sequence 31, Appl
37	15	100.0	32	10	US-09-977-406a-26	Sequence 32, Appl
38	15	100.0	32	10	US-09-977-406a-75	Sequence 33, Appl
39	15	100.0	33	10	US-09-977-406a-27	Sequence 34, Appl
40	15	100.0	33	10	US-09-977-406a-76	Sequence 35, Appl
41	15	100.0	34	10	US-09-977-406a-28	Sequence 36, Appl
42	15	100.0	34	10	US-09-977-406a-77	Sequence 37, Appl
43	15	100.0	35	10	US-09-977-406a-29	Sequence 38, Appl
44	15	100.0	35	10	US-09-977-406a-78	Sequence 39, Appl
45	15	100.0	36	10	US-09-977-406a-30	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-977-406a-5
; Sequence 5, Application US/09977406a
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCOYON PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCK3145 (polypeptide 31-45)
US-09-977-406a-5
Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 EMQDNCETCTCYET 15
Db 1 EMQDNCETCTCYET 15
RESULT 2
US-10-291-360-5
; Sequence 5, Application US/10291360

Publication No. US20030119744A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-051-US-02
CURRENT APPLICATION NUMBER: US/10/291,360
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCK3145 (polypeptide 31-45)
US-10-291-360-5

Query Match 100.0%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYET 15
Db 1 EWQTDNCETCTCYET 15

RESULT 3
US-10-857-358-5
Sequence 5, Application US/10857358
Publication No. US2005002683A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-153
CURRENT APPLICATION NUMBER: US/10/857,358
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 10/291,360
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCK3145 (polypeptide 31-45)
US-10-857-358-5

Query Match 100.0%; Score 15; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYET 15
Db 1 EWQTDNCETCTCYET 15

RESULT 4
US-09-977-406A-10
Sequence 10, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-10

Query Match 100.0%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYET 15
Db 1 EWQTDNCETCTCYET 15

RESULT 5
US-09-977-406A-59
Sequence 59, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-59

Query Match 100.0%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYET 15
Db 2 EWQTDNCETCTCYET 16

RESULT 6
US-09-977-406A-11
Sequence 11, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 17
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-11

Query Match 100.0%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
Db 1 EMQDNCETCTCYET 15

RESULT 7
US-09-977-406a-60
Sequence 60, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-60.

Query Match 100.0%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
Db 3 EMQDNCETCTCYET 17

RESULT 8
US-09-977-406a-12
Sequence 12, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-12

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQDNCETCTCYET 15
Db 1 EMQDNCETCTCYET 15

RESULT 9
US-09-977-406a-61
Sequence 61, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-61

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
Db 4 EMQDNCETCTCYET 18

RESULT 10
US-09-977-406a-13
Sequence 13, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406a-13

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYET 15
Db 1 EMQDNCETCTCYET 15

RESULT 11
US-09-977-406A-62
; Sequence 62, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 62
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-62

Query Match 100.0%; Score 15; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQTDNCETCTCYET 15
DB 5 EWQTDNCETCTCYET 19

RESULT 12
US-09-977-406A-14
; Sequence 14, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-14

Query Match 100.0%; Score 15; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQTDNCETCTCYET 15
DB 1 EWQTDNCETCTCYET 15

RESULT 13
US-09-977-406A-63
; Sequence 63, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS

; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 63
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-63

Query Match 100.0%; Score 15; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQTDNCETCTCYET 15
DB 6 EWQTDNCETCTCYET 20

RESULT 14
US-09-977-406A-15
; Sequence 15, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 15
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-15

Query Match 100.0%; Score 15; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQTDNCETCTCYET 15
DB 1 EWQTDNCETCTCYET 15

RESULT 15
US-09-977-406A-64
; Sequence 64, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20


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; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 64
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-64

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Query Match      100.0%; Score 15; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  EMQTDNCETCTCYET 15
          |||||
Db      7  EMQTDNCETCTCYET 21

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Search completed: May 4, 2005, 15:24:07
 Job time : 17.7455 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:12:38 ; Search time 5.4 Seconds
(without alignments)
267.269 Million cell updates/sec

Title: US-09-977-406A-5

Sequence: 1 EMQDNCETCTCYET 15

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	114	2 A34567	beta-microseminop
2	6	40.0	326	2 UC7094	nine-heme cytochr
3	6	40.0	601	2 B96744	unknown protein [i
4	6	40.0	895	2 T32374	hypothetical prote
5	5	33.3	38	2 JN0613	defensin 4K - scor
6	5	33.3	38	2 S27242	defensin - blue da
7	5	33.3	83	2 S53116	methionine adenosy
8	5	33.3	91	2 S52089	transcription fact
9	5	33.3	114	2 A54663	seminal plasma pro
10	5	33.3	119	1 S73864	hypothetical prote
11	5	33.3	130	2 G65019	hypothetical prote
12	5	33.3	167	2 C86241	protein T16B5.9 [i
13	5	33.3	210	2 AC2316	transposase alr408
14	5	33.3	246	2 A81679	conserved hypochet
15	5	33.3	295	2 S76790	hypothetical prote
16	5	33.3	301	2 T26546	hypothetical prote
17	5	33.3	319	1 T50370	transcription fact
18	5	33.3	322	2 C70905	hypothetical prote
19	5	33.3	334	2 D82803	glyceraldehyde-3-p
20	5	33.3	340	1 B55973	transcription fact
21	5	33.3	347	2 AC0825	anaerobic sulfite
22	5	33.3	348	2 A38453	transcription fact
23	5	33.3	349	1 T50369	transcription fact
24	5	33.3	358	1 A55973	transcription fact
25	5	33.3	358	1 T51735	transcription fact
26	5	33.3	359	1 T51734	transcription fact
27	5	33.3	360	1 A55198	transcription fact
28	5	33.3	360	2 T06592	methionine adenosy
29	5	33.3	361	2 T50505	gene wnt8 protein

30	5	33.3	363	1 C55973	transcription fact
31	5	33.3	366	2 S66351	methionine adenosy
32	5	33.3	374	2 S41758	heat shock protein
33	5	33.3	374	2 C97058	molecular chaperon
34	5	33.3	390	2 S46540	methionine adenosy
35	5	33.3	390	2 S49491	methionine adenosy
36	5	33.3	390	2 G84785	probable s-adenosy
37	5	33.3	391	2 T43318	YNL123w protein ho
38	5	33.3	393	2 S38875	methionine adenosy
39	5	33.3	393	2 S46358	methionine adenosy
40	5	33.3	393	2 JN0131	methionine adenosy
41	5	33.3	393	2 C86155	S-adenosylmethioni
42	5	33.3	393	2 J00410	methionine adenosy
43	5	33.3	394	2 T06180	methionine adenosy
44	5	33.3	396	2 T10710	methionine adenosy
45	5	33.3	397	2 S66352	methionine adenosy

ALIGNMENTS

RESULT 1
A34567
beta-microseminoprotein precursor - human
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma prc
C:Species: Homo sapiens (hmn)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C/Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682
R/Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
A/Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein ge
A/Reference number: A34567; MUID:90211299; PMID:232265
A/Accession: A34567
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-114 <GRE>
A/Cross-references: UNIPROT:P08118; GB:M34376; NID:G514370; PIDN:AAA59871.1; PID:G514372
R/Milkey, M.; Nollet, S.; Fournier, S.; Benjannet, S.; Chappdelaine, P.; Paradis, G.; Dube,
DNA 6, 23-29, 1987
A/Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma pr
A/Reference number: A26451; MUID:87161231; PMID:3829888
A/Accession: A26451
A/Molecule type: mRNA
A/Residues: 1-114 <MEI>
A/Cross-references: GB:M15885; NID:G338414; PIDN:AAA3635.1; PID:G338415
R/Akiyama, K.; Yoshioaka, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara, M
Biochim. Biophys. Acta 829, 288-294, 1985
A/Title: The amino acid sequence of human beta-microseminoprotein.
A/Reference number: A29777; MUID:85199974; PMID:3995056
A/Accession: A29777
A/Molecule type: protein
A/Residues: 21-58, 'PR', 61-113 <AKI>
R/Seidah, N.G.; Arbach, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.
FEBS Lett. 175, 349-355, 1984
A/Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction of
A/Reference number: A30984; MUID:85004133; PMID:6434350
A/Accession: A30984
A/Molecule type: protein
A/Residues: 21-112, 'G', 114 <SEI>
R/Weiber, H.; Anderson, C.; Murne, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
Am. J. Pathol. 137, 593-604, 1990
A/Title: Beta microseminoprotein is not a prostate-specific protein.
A/Reference number: A60673; MUID:90379237; PMID:2205099
A/Accession: A60673
A/Molecule type: protein
A/Residues: 21, 'X', 23-34 <MEI>
R/Nollet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A/Reference number: S16237; MUID:91274357; PMID:2054385
A/Accession: S16238
A/Molecule type: DNA

A/Residues: 1-114 <NOL>
A/Cross-references: EMBL:X57928; NID:935760; PIDN:CAA41002.1; PID:9825707
A/Note: the authors translated the codon ACT for residue 54 as Trp
R/Rev: A.Y.; Brainer, R.C.; Vessella, R.L.
Cancer Lett. 74, 91-99, 1993
A/Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.
A/Reference number: 152682; PMID:94115955; PMID:7506990
A/Accession: 152682
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-114 <RES>
A/Cross-references: GB:S67815; NID:9460568; PIDN:AAB29732.1; PID:9460569
A/Comment: This protein is a component of seminal plasma as well as secretory fluids from
C/genetics:
A/Genes: GDB:MSMB
A/Cross-references: GDB:128042; OMIM:157145
A/Map position: 10q11.2-10q11.2
A/Intons: 1/3; 37/1; 72/2
C/Superfamily: seminal plasma protein
C/Keywords: semen
F/1-20/Domains: signal sequence #status predicted <SIG>
F/21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 100.0%; Score 6; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 4, 6e-11;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMOTDNCETCTCCT 15
DB 51 EMOTDNCETCTCCT 65

RESULT 2

JC7094
nine-heme cytochrome c - Desulfovibrio desulfuricans
C/Species: Desulfovibrio desulfuricans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: JC7094
R/Saraiya, L.M.; da Costa, P.N.; Legall, J.
Biochem. Biophys. Res. Commun. 262, 629-634, 1999
A/Title: Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774 nine-heme c
A/Reference number: JC7094; PMID:99400423; PMID:10471375
A/Accession: JC7094
A/Molecule type: DNA
A/Residues: 1-326 <SAR>
A/Cross-references: UNIPROT:Q9RNE8; GB:AF186393; NID:95924394; PIDN:AAD56586.1; PID:9592
A/Experimental source: ATCC 27774
C/genetics:
A/Genes: 9HCC
C/Keywords: electron transfer; heme; heme binding

Query Match 40.0%; Score 6; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 4, 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 DNCETC 10
DB 75 DNCETC 80

RESULT 3

B96744
unknown protein (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: B96744
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maich, R.; Matzli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; PMID:21016719; PMID:11130712
A/Accession: B96744
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-601 <STO>

A/Cross-references: UNIPROT:Q9C7H2; GB:AE005173; NID:911054407; PIDN:AAG27794.1; GSPDB:G
C/genetics:
A/Genes: F28P5.4
A/Map position: 1

Query Match 40.0%; Score 6; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 7, 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CETCTC 12
DB 514 CETCTC 519

RESULT 4

T32374
hypothetical protein K10F12.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
C/Accession: T32374
R/Woldmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A/Description: The sequence of C. elegans cosmid K10F12.
A/Reference number: Z21157
A/Accession: T32374
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-895 <WOL>
A/Cross-references: EMBL:AF025462; PIDN:AAB71005.1; GSPDB:GN00021; CESP:K10F12.3
A/Experimental source: strain Bristol N2; clone K10F12
C/genetics:
A/Genes: CESP:K10F12.3
A/Map position: 3
A/Intons: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 624
C/Superfamily: Yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phospho
sphodiesterase domain Y homology
F/338-487/Domains: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 40.0%; Score 6; DB 2; Length 895;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TDNCET 9
DB 288 TDNCET 293

RESULT 5

JN0613
defensin 4K - scorpion (leirurus quinquestratus)
N/Alternate names: antibacterial 4K peptide
C/Species: Leirurus quinquestratus hebraeus
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0613
R/Cocianciuc, S.; Goyffon, M.; Bontems, F.; Bulet, P.; Bouet, F.; Menez, A.; Hoffmann, J.
Biochem. Biophys. Res. Commun. 194, 17-22, 1993
A/Title: Purification and characterization of a scorpion defensin, a 4kDa antibacterial p
A/Reference number: JN0613; PMID:93326112; PMID:8333834
A/Accession: JN0613
A/Molecule type: protein
A/Residues: 1-38 <COC>

A/Cross-references: UNIPROT:P41965
A/Note: this protein is similar to scorpion toxins and insect defensins

Query Match 33.3%; Score 5; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13
Db 32 TCTCY 36

RESULT 6

S27242
defensin - blue darter
C/Species: Aeschna cyanea (blue darter)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S27242
R/Bulet, P.; Cociancich, S.; Reuland, M.; Sauber, F.; Bischoff, R.; Hegy, G.; van Dorssse
Eur. J. Biochem. 209, 977-984, 1992
A/Title: A novel insect defensin mediates the inducible antibacterial activity in larvae
A/Reference number: S27242; MUID:91049356; PMID:1425705
A/Accession: S27242
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-38 <BU>
A/Cross-references: UNIPROT:P80154

Query Match 33.3%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13
Db 33 TCTCY 37

RESULT 7

S53116
methionine adenosyltransferase (EC 2.5.1.6) - chickpea (fragment)
N/Alternate names: S-adenosylmethionine synthetase
C/Species: Cicer arietinum (chickpea, garbanzo)
C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S53116
R/Cervantes, E.
submitted to the EMBL Data Library, March 1995
A/Reference number: S53116
A/Accession: S53116
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-83 <CER>
A/Cross-references: UNIPROT:Q39465; EMBL:X85252; NID:G1808591; PIDN:CAA59508.1; PID:G732
C/Superfamily: methionine adenosyltransferase
C/Keywords: S-adenosylmethionine; transferase

Query Match 33.3%; Score 5; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CECTCT 11
Db 43 CECTCT 47

RESULT 8

S52089
transcription factor isl-2a (clone S3) - chinook salmon
N/Alternate names: insulin enhancer-binding protein isl-2a; islet-2a protein
C/Species: Oncorhynchus tshawytscha (chinook salmon)
C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C/Accession: S52089
R/Gong, Z.; Hew, C.L.
Biochim. Biophys. Acta 1260, 349-354, 1995
A/Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus tshawytscha)
A/Reference number: S52089; MUID:95178560; PMID:7873614
A/Accession: S52089
A/Molecule type: mRNA

A/Residues: 1-91 <GON>
A/Cross-references: EMBL:X64882
A/Experimental source: clone S3
C/Genetics:

A/Gene: isl-2a
C/Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat h
C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F/3-56/Domain: LIM metal-binding repeat homology <LIM>

Query Match 33.3%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ETCCTC 12
Db 40 ETCCTC 44

RESULT 9

A54663
seminal plasma protein PSP-94 precursor - rhesus macaque
N/Alternate names: prostatic secretory protein PSP94
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C/Accession: S16237; A54663
R/Nolet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A/Reference number: S16237; MUID:91274357; PMID:2054385
A/Accession: S16237
A/Molecule type: DNA
A/Residues: 1-114 <NO2>

A/Cross-references: UNIPROT:P25142; EMBL:X57932; NID:G38094; PIDN:CAA41003.1; PID:G82915
A/Note: the authors translated the codon ACT for residue 54 as Ttp
R/Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.
Genomics 9, 775-777, 1991

A/Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence bet
A/Reference number: A54663; MUID:91244325; PMID:2037304
A/Accession: A54663
A/Molecule type: mRNA

A/Residues: 1-114 <NOL>
A/Cross-references: GB:M92161; NID:G342280; PIDN:AAA36903.1; PID:G342281
C/Genetics:

A/Introns: 1/3; 37/1; 72/2
C/Superfamily: seminal plasma protein
F/1-20/Domain: signal sequence #status predicted <SIG>

Query Match 33.3%; Score 5; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8
Db 54 TDNCE 58

RESULT 10

S73864
hypothetical protein H10 orf19 - Mycoplasma pneumoniae (strain ATCC 29342)
C/Species: Mycoplasma pneumoniae
A/Variety: ATCC 29342
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S73864
R/Himmelsreich, R.; Hilbert, H.; Plagens, H.; Pirk1, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
A/Reference number: S73327; MUID:97105885; PMID:8948633
A/Accession: S73864
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-119 <HIM>
A/Cross-references: UNIPROT:P75480; EMBL:AE000052; GB:U00089; NID:G1674223; PIDN:AAB9618
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C/Genetics:
A:Genetic code: SGC3
C:Superfamily: holo-ACP synthase

Query Match 33.3%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTDNC 7
Db 21 QTDNC 25

RESULT 11

G65019
hypothetical protein b2448 - Escherichia coli (strain K-12)

C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C/Accession: G65019

R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:9742617; PMID:9278503

A/Accession: G65019

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-110 <BLAT>

A/Cross-references: UNIPROT:P76548; GB:AE000332; GB:U00096; NID:g1788789; PIDN:AACT5501.

A/Experimental source: strain K-12, substrain MG1655

C:Superfamily: Escherichia coli hypothetical protein b2448

Query Match 33.3%; Score 5; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8
Db 43 TDNCE 47

RESULT 12

C86241
protein T16B5.9 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cross)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C/Accession: C86241

R/Theologis, A.; Ecker, J.R.; Palm, C.T.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luross, J.S.; Maiz, R.; Matzali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: C86241

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-167 <STO>

A/Cross-references: UNIPROT:Q9SAC5; GB:AE005172; NID:g4874271; PIDN:AAD31336.1; GSPDB:GN

C/Genetics:

A:Gene: T16B5.9

A/Map position: 1

Query Match 33.3%; Score 5; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCYET 15
|||||

Db 91 TCYET 95

RESULT 13

AC2316

transposase alr4082 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C/Accession: AC2316

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AC2316

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-210 <KUR>

A/Cross-references: UNIPROT:Q8YFV8; GB:BA000019; PIDN:BA875781.1; PID:g17133217; GSPDB:GN

A/Experimental source: strain PCC 7120

C/Genetics:

A:Gene: alr4082

Query Match 33.3%; Score 5; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQTD 5
Db 111 EWQTD 115

RESULT 14

AB1679

conserved hypothetical protein TC0662 [imported] - Chlamydia muridarum (strain Nigg)

C/Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: AB1679

R/Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I
.C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000

A/Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A/Reference number: AB1500; MUID:20150255; PMID:1064935

A/Accession: AB1679

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-246 <TET>

A/Cross-references: UNIPROT:Q9PK11; GB:AE002334; GB:AE002160; NID:g7190690; PIDN:AAF3948E

A/Experimental source: strain Nigg (MoPn)

C/Genetics:

A:Gene: TC0662

Query Match 33.3%; Score 5; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCYET 15
Db 198 TCYET 202

RESULT 15

S76790

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C/Species: Synechocystis sp.

A/Variety: PCC 6803

C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S76790

R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O.K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996

A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

9.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S76790
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-295 <KAN>
 A;Cross-references: UNIPROT:P74594; EMBL:D90916; GB:AB001339; NID:G1653715; PIDN:BAA1870
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Start codon: GTG
 C;Superfamily: fructosamine kinase

Query Match 33.3%; Score 5; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 WOTDN 6
 |||||
 Db 132 WOTDN 136

Search completed: May 4, 2005, 14:34:53
 Job time : 5.4 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:04:27 ; Search time 25.7455 Seconds

(without alignments)
298.351 Million cell updates/sec

Title: US-09-977-406a-5

Sequence: 1 EMQDNCCTCTCYET 15

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	114	1 MSMB_HUMAN	P08118 homo sapien
2	7	46.7	114	1 MSMB_PAPAN	O28767 mus anubii
3	6	40.0	196	1 Q9D8Y1	O96891 mus musculus
4	6	40.0	326	1 CTC9_DESDE	O9rm68 desulfovibr
5	6	40.0	459	1 MURD_LACPL	O98v80 lactobacilli
6	6	40.0	601	2 Q9C7H2	O9c7h2 arabidopsis
7	6	40.0	1068	2 O8IA76	O8ia76 caenorhabdi
8	6	40.0	1075	2 O8IA75	O8ia75 caenorhabdi
9	6	40.0	1615	2 Q7QZU9	O7qzu9 giardia lam
10	6	40.0	1870	2 Q7OH34	O7oh34 fowlpox vir
11	6	40.0	1870	2 Q9J5A0	O9j5a0 fowlpox vir
12	6	40.0	3110	1 LMA2_HUMAN	P24043 homo sapien
13	5	33.3	37	1 DEF4_LACPL	P56686 drosophila
14	5	33.3	38	1 DEF4_LACPL	P41965 leucis qui
15	5	33.3	38	1 DEF1_AESCY	P60154 aescina cya
16	5	33.3	51	2 Q7Y3N1	O7y3n1 enterobacte
17	5	33.3	54	2 Q24985	O24985 giardia lam
18	5	33.3	58	2 O8FCX2	O8fcx2 escherichia
19	5	33.3	70	2 O6R5C3	O6r5c3 mus musculu
20	5	33.3	74	1 DEF1_DERVA	O86q15 dermatocent
21	5	33.3	74	2 O86LE4	O86le4 boophilus m
22	5	33.3	75	2 O8JX66	O8jx66 sen virus.
23	5	33.3	75	2 O8JX67	O8jx67 sen virus.
24	5	33.3	83	2 Q39465	O39465 cicler arlet
25	5	33.3	105	2 O8BU77	O8bu77 mus musculu
26	5	33.3	110	2 Q421C9	O421c9 arabidopsis
27	5	33.3	111	2 Q9JH97	O9jh97 unclassified
28	5	33.3	112	2 O854B7	O854b7 mycobacteri
29	5	33.3	113	2 O22079	O22079 nicotiana t
30	5	33.3	114	1 MSMB_MACMU	P51142 macaca mula
31	5	33.3	115	2 Q7KTX0	O7ktx0 drosophila

32	5	33.3	119	1 ACP5_MYCPN	P75480 mycoplasma
33	5	33.3	127	2 O6IKD4	O6ikd4 drosophila
34	5	33.3	130	1 YPFO_ECOLI	P76548 escherichia
35	5	33.3	131	2 O8CFE4	O8cfe4 mus musculu
36	5	33.3	132	2 O97442	O97442 giardia lam
37	5	33.3	137	2 Q24987	O24987 giardia lam
38	5	33.3	137	2 Q9W101	O9w101 drosophila
39	5	33.3	149	2 Q7PS82	O7ps82 anopheles g
40	5	33.3	151	2 Q9UG32	O9ug32 homo sapien
41	5	33.3	151	2 Q9FT84	O9ft84 arabidopsis
42	5	33.3	161	2 Q93L46	O93l46 bacteroides
43	5	33.3	164	2 O8LRJ3	O8lrj3 oryza sativ
44	5	33.3	167	2 O8LDL5	O8ldl5 arabidopsis
45	5	33.3	167	2 Q9SACS	O9sacs arabidopsis

ALIGNMENTS

RESULT 1
MSMB_HUMAN STANDARD; PRT; 114 AA.
ID MSMB_HUMAN
AC P08118; P11999; Q13125; Q9UCS9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (immunoglobulin binding factor) (IGBF) (PN44).
DE Name=MSMB; Synonyms=PRSP;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=67161231; PubMed=3829888;
RX Molkay M., Nole S., Fournier S., Benjannet S., Chapelaine P., Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidah N.G., Chretien M.;
RA "Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma protein secreted by the human prostate.";
RT DNA 6:23-29(1987).
RN [2]
RP MEDLINE=91274357; PubMed=2054385; DOI=10.1016/0167-4781(91)90016-F;
RX Nole S., Molkay M., Chretien M.;
RA "Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";
RT Biochim. Biophys. Acta 1089:247-249(1991).
RN [3]
RP MEDLINE=90211299; PubMed=2322265;
RX Green C.B., Liu W.Y., Kwok S.C.M.;
RA "Cloning and nucleotide sequence analysis of the human beta-microseminoprotein gene.";
RT Biochem. Biophys. Res. Commun. 167:1184-1190(1990).
RN [4]
RP MEDLINE=90073664; PubMed=2590204;
RX Uvshbeck M., Lindstrom C., Welber H., Abrahamson P.-A., Lilja H., Lundwall A.;
RA "Molecular cloning of a small prostate protein, known as beta-microseminoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in non-genital tissues.";
RT Biochem. Biophys. Res. Commun. 164:1310-1315(1989).
RN [5]
RP MEDLINE=94115955; PubMed=7506990; DOI=10.1016/0304-3835(93)90049-F;
RX Liu A.Y., Bradner R.C., Vessella R.L.;
RA "Decreased expression of prostatic secretory protein PSP94 in prostate cancer.";
RT

RT Cancer Lett. 74:91-99(1993).
RN [61]
RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC TISSUE=Prostate;
RX MEDLINE=96032566; PubMed=7566962;
RA Xian J.W., Chin J.L., Guo Y., Chambers A.F., Finkelman M.A.,
RA Clarke M.W.;
RT "Alternative splicing of PSP4 (prostatic secretory protein of 94
RT amino acids) mRNA in prostate tissue.";
RL Oncogene 11:1041-1047(1995).
RN [7]
RP SEQUENCE FROM N.A.
RA Baijal-Gupta M., Clarke M.W.;
RT "Prostate specific protein (PSP4) expression in a human endometrial
RT cell line (KLE3)." ;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bietow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casarini T.L., Schetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., Morley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 2-72 FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein." ;
RL Eur. J. Biochem. 264:407-414(1999).
RN [10]
RP SEQUENCE OF 21-113.
RX MEDLINE=85199974; PubMed=3995056; DOI=10.1016/0167-4838(85)90200-6;
RA Akiyama K., Yoshitaka Y., Schmid K., Offner G.D., Troxler R.F.,
RA Tsuda R., Hara M.;
RT "The amino acid sequence of human beta-microseminoprotein." ;
RL Biochim. Biophys. Acta 829:288-294(1985).
RN [11]
RP SEQUENCE OF 21-114.
RX MEDLINE=85004133; PubMed=6434350; DOI=10.1016/0014-5793(84)80766-8;
RA Seihah N.G., Arbatli N.J., Rochemont J., Sheh A.R., Chretien M.;
RT "Complete amino acid sequence of human seminal plasma beta-inhibin.
RT Prediction of post Gln-Arg cleavage as a maturation site." ;
RL FEBS Lett. 173:349-355(1984).
RN [12]
RP SEQUENCE OF 21-50 AND 113-114.
RX MEDLINE=9208964; PubMed=1930232;
RA Liang Z.G., Kamada M., Koide S.S.;
RT "Structural identity of immunoglobulin binding factor and prostatic
RT secretory protein of human seminal plasma." ;
RL Biochem. Biophys. Res. Commun. 180:356-359(1991).
RN [13]
RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.
RX MEDLINE=95401076; PubMed=7671139; DOI=10.1016/1357-2725(95)00021-G;
RA Ohkubo I., Tada T., Ochiai Y., Ueyama H., Shimoto T., Sasaki M.;

RT "Human seminal plasma beta-microseminoprotein: its purification,
RT characterization, and immunohistochemical localization." ;
RL Int. J. Biochem. Cell Biol. 27:603-611(1995).
RN [14]
RP SEQUENCE OF 21-32.
RX MEDLINE=21648993; PubMed=11788998;
RA DOI=10.1002/1615-9861(200201)21:1<112::AID-PROT112>3.3.CO;2-E;
RA Ghatouari B., Stahlbom B., Tagesson C., Lindahl M.;
RT "Newly identified proteins in human nasal lavage fluid from non-
RT smokers and smokers using two-dimensional gel electrophoresis and
RT peptide mass fingerprinting." ;
RL Proteomics 2:112-120(2002)
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=PSP94;
CC IsoId=P08118-1; Sequence=Displayed;
CC Name=PSP57;
CC -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,
CC breast and penis. Also expressed in pancreas, esophagus, stomach,
CC duodenum, colon, trachea, lung, salivary glands and fallopian
CC tube. PSP94 is expressed in lung and breast, whereas PSP57 is
CC found in kidney and bladder.
CC -1- MISCELLANEOUS: Specific receptors for this protein are found on
CC spermatozoa and in the prostate.
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -1- CAUTION: Was originally thought to inhibit the secretion of FSH by
CC pituitary cells.

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DR EMBL, M34376; AA59871.1; -
DR EMBL, M34373; AA59871.1; JOINED.
DR EMBL, M34374; AA59871.1; JOINED.
DR EMBL, M34375; AA59871.1; JOINED.
DR EMBL, M15885; AA36635.1; -
DR EMBL, X57928; CAA41002.1; -
DR EMBL, X57929; CAA41002.1; JOINED.
DR EMBL, X57930; CAA41002.1; JOINED.
DR EMBL, X57931; CAA41002.1; JOINED.
DR EMBL, S67815; AAB29732.1; -
DR EMBL, U22178; AA83556.1; -
DR EMBL, U78976; AAB37355.1; -
DR EMBL, BC005257; AAH05257.1; -
DR EMBL, A0133356; CAB39325.1; -
DR PIR, A34567; A34567.
DR PIR, G01730; G01730.
DR H-InvDB, HIX0008822; -
DR GeneW, HGNC:7372; MSMB.
DR MIM, 157145; -
DR GO, GO:0005615; C:extracellular space; TAS.
DR GO, GO:0005634; C:nucleus; TAS.
DR InterPro, IPR008735; PSP94.
DR Pfam, PF05825; PSP94; 1.
KW Alternative splicing; Direct protein sequencing; Polymorphism; Signal.
FT SIGNAL 1 20
FT CHAIN 21 114
FT DIULFID 22 38
FT DIULFID 57 93
FT DIULFID 60 69
FT DIULFID 62 70
FT DIULFID 84 107
FT VASPLIC 37 77

FT By similarity.
FT Or C-60 with C-70 (By similarity).
FT Or C-62 with C-69 (By similarity).
FT By similarity.
FT KMDIKGNKPKINSQWQNDQNCCTCTCTETISCTLVSTPV
FT -> MFLHWVWTKTKAESRRRTASTSMWRRTQKQPVLS
FT VNG (in isoform PSP57).
FT /FtId=VSP_003275.

```

FT VARSPIC 78 114 Missing (in isoform PSP57) .
FT FT /FTid=VSP_003276.
Query Match 100.0%; Score 15; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. NO. 1.3e-10;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMOTNCECTCYET 15
DB 51 EMOTNCECTCYET 65

RESULT 2
MSMB PAPAN STANDARD; PRT; 114 AA.
AC Q28767;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
DE protein) (Prostate secretory protein PSP94) (PSP-94).
GN Name=MSMB; Synonyms=PSP94;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OC NCBI_Taxid=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=97316893; PubMed=9174167;
RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mbikay M., Zhong R.,
RA Chiu J.L.;
RT "Molecular cloning and gene expression analysis of PSP94 (prostate
RT secretory protein of 94 amino acids) in primates.";
RL DNA Cell Biol. 16:627-638(1997).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC
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CC -----
DR EMBL; U49786; AAB62726.1; -
DR InterPro: IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
KW signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 114 Beta-microseminoprotein.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.
FT DISULFID 60 69 Or C-60 with C-70 (By similarity).
FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT DISULFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 13013 MW; A08C837BD81F98BD CRC64;

Query Match 46.7%; Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. NO. 0.54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 WOTDNCE 8
DB 52 WOTDNCE 58

RESULT 3
Q9DBY1 PRELIMINARY; PRT; 196 AA.
AC Q9DBY1;

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DT 01-JUN-2001 (TRENBLERel. 17, Created)
DT 01-JUN-2001 (TRENBLERel. 17, Last sequence update)
DT 25-OCT-2004 (TRENBLERel. 28, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:1810020E01 product:hypothetical protein, full insert
DE sequence (RIKEN CDNA 1810020E01).
GN Name=1810020E01Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RT Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RT Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT "Normalization and subfraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishogi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoaka T., Hori F.,
RA Imotoi K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yamashita A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.

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RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D.,
RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Mustatina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci T., Prange C.,
RA Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RM [8].
RP
RC SEQUENCE FROM N.A.
RC STRAIN=FVE/N; TISSUE=Mammary tumor. C3;
RC Strausberg R.;
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007559; BAB25107.1; -.
DR MGI; BC023171; AAH23171.1; -.
DR EMBL; MGI:1913521; 1810020E01Rik.
GO: GO:0016021; C:Integral to membrane; TAS.
DR InterPro; IPR009801; DUF1370.
DR Pfam; PF07114; DUF1370; 1.
KW Hypothetical protein.
SQ
SEQUENCE 196 AA; 21539 MW; 994DF5E2521C5FEB CRC64;

Query Match 40.0%; Score 6; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 98 NCERTCT 103

RESULT 4
CYC9_DESDE
AC Q9RNB6; STANDARD; PRT; 326 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DS Nine-heme cytochrome c precursor (9Hcc).
OS Desulfovibrio desulfuricans.
OC Bacteria; Proteobacteria; Delta proteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=876;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27774;
RC MEDLINE=99400423; PubMed=10471375; DOI=10.1006/bbrc.1999.1238;
RA Saraiva L.M., da Costa P.N., Legall J.;
RT "Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774
RT nine-heme cytochrome c.";
RL Biochem. Biophys. Res. Commun. 262:629-634(1999).
RM [2].
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RC STRAIN=ATCC 27774;
RC MEDLINE=20022508; PubMed=10555582;
RA Matias P.M., Saraiva L.M., Soares C.M., Coelho A.V., Legall J.,
RA Garrondo M.A.;
RT "Nine-haem cytochrome c from Desulfovibrio desulfuricans ATCC 27774:
RT primary sequence determination, crystallographic refinement at 1.8 A

```

RT	c3";
RT	and modelling studies of its interaction with the tetrahaem cytochrome
RL	J. Biol. Inorg. Chem. 4:478-494(1999).
RN	[3]
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RC	STRAIN=ATCC 27774;
RX	MEDLINE=99148120; PubMed=10368280; DOI=10.1016/S0969-2126(99)80019-7;
RA	Matias P.M., Coelho R., Pereira I.A.C., Coelho A.V., Thompson A.W.,
RA	Siekier L., Jégali J., Carrondo M.A.;
RT	"The primary and three-dimensional structures of a nine-haem
RT	cytochrome c from Desulfotomobium desulfuricans ATCC 27774 reveal a new
RL	member of the hmc family.";
RL	Structure 7:119-130(1999).
CC	-I- FUNCTION: May form part of a transmembrane redox complex through
CC	which electrons are transferred to the cytoplasm for reduction of
CC	sulfate.
CC	-I- SUBUNIT: Monomer.
CC	-I- SUBCELLULAR LOCATION: Periplasmic.
CC	-I- DOMAIN: Arranged into two tetraheme clusters and the extra heme 4
CC	is located asymmetrically between the two regions.
CC	-I- PTM: Binds 9 heme groups per subunit.
CC	-I- SIMILARITY: Contains 9 cytochrome c domains.
CC	-----
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CC	-----
DR	EMBL, AF186393, AA056586.1; .
DR	PIR, JC7094, JC7094.
DR	PDB, 1PHC; X-ray; A/B=31-322.
DR	PDB, IOFH; X-ray; A/B=31-326.
DR	PDB, IOFY; X-ray; A/B=31-326.
DR	InterPro, IPRO00345; Cytc_heme_BS.
DR	InterPro, IPRO02322; Cyt_CITR.
DR	InterPro, IPR011031; Multihem_cyt.
DR	Pfam, PF02085; Cytochrom_CIT1; 1.
DR	PRINTS, PR00609; CYTOCHROME_C3.
DR	PROSITE, PS51008; MULTIHEME_CYTC_1.
KV	3D-structure; Electron transport; Heme; Periplasmic; Repeat; Signal.
FT	SIGNAL 1 30
FT	CHAIN 31 326
FT	METAL 67 67 Nine-heme cytochrome C.
FT	METAL 70 70 Iron (heme 1 axial ligand).
FT	BINDING 77 77 Iron (heme 3 axial ligand).
FT	BINDING 80 80 Heme 1 (covalent).
FT	METAL 81 81 Heme 1 (covalent).
FT	METAL 82 81 Iron (heme 1 axial ligand).
FT	BINDING 89 89 Iron (heme 2 axial ligand).
FT	BINDING 92 92 Heme 2 (covalent).
FT	METAL 93 93 Heme 2 (covalent).
FT	METAL 111 111 Iron (heme 2 axial ligand).
FT	BINDING 127 130 Iron (heme 5 axial ligand).
FT	BINDING 130 130 Heme 3 (covalent).
FT	METAL 131 131 Heme 3 (covalent).
FT	BINDING 141 141 Iron (heme 3 axial ligand).
FT	BINDING 144 144 Heme 4 (covalent).
FT	METAL 145 144 Heme 4 (covalent).
FT	BINDING 157 157 Iron (heme 4 axial ligand).
FT	BINDING 160 160 Heme 5 (covalent).
FT	BINDING 161 161 Heme 5 (covalent).
FT	METAL 227 227 Iron (heme 5 axial ligand).
FT	METAL 230 230 Iron (heme 6 axial ligand).
FT	METAL 248 248 Iron (heme 8 axial ligand).
FT	BINDING 255 255 Iron (heme 4 axial ligand).
FT	BINDING 258 258 Heme 6 (covalent).
FT	METAL 259 259 Heme 6 (covalent).
FT	METAL 260 260 Iron (heme 6 axial ligand).
FT	METAL 271 271 Iron (heme 7 axial ligand).
FT	BINDING 274 274 Heme 7 (covalent).
FT	BINDING 274 274 Heme 7 (covalent).

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FT METAL 275 275 Iron (heme 7 axial ligand).
FT METAL 294 294 Iron (heme 9 axial ligand).
FT BINDING 297 297 Heme 8 (covalent).
FT BINDING 300 300 Heme 8 (covalent).
FT METAL 301 301 Iron (heme 8 axial ligand).
FT BINDING 314 314 Heme 9 (covalent).
FT BINDING 317 317 Heme 9 (covalent).
FT METAL 318 318 Iron (heme 9 axial ligand).
FT STRAND 43 46
FT STRAND 55 56
FT STRAND 63 66
FT HELIX 67 73
FT HELIX 77 80
FT TURN 82 83
FT HELIX 89 91
FT TURN 92 92
FT HELIX 99 101
FT TURN 102 103
FT HELIX 106 111
FT HELIX 127 137
FT HELIX 139 142
FT TURN 143 143
FT HELIX 144 147
FT HELIX 154 160
FT STRAND 161 161
FT TURN 165 166
FT HELIX 169 177
FT TURN 178 178
FT HELIX 182 195
FT HELIX 204 206
FT STRAND 211 213
FT TURN 215 216
FT STRAND 220 220
FT STRAND 223 225
FT HELIX 227 236
FT TURN 237 240
FT HELIX 242 247
FT TURN 251 252
FT HELIX 253 257
FT TURN 258 258
FT HELIX 271 274
FT TURN 281 282
FT TURN 284 285
FT HELIX 289 303
FT TURN 304 305
FT TURN 311 312
FT STRAND 320 320
SQ SEQUENCE 326 AA; 35025 MW; 2ED7025ADDF250E3 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RN [1]
SEQUENCE FROM N.A.
RP STRAIN=NCIMB 8826 / WCFS1;
RC MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RX Kleebebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
-1- FUNCTION: Cell wall formation. Catalyzes the addition of glutamate
to the nucleotide precursor UDP-N-acetyl[muramoyl-L-alanine (UMA)
(BY similarity).
-1- CATALYTIC ACTIVITY: ATP + UDP-N-acetyl[muramoyl-L-alanine +
glutamate = ADP + phosphate + UDP-N-acetyl[muramoyl-L-alanyl-D-
glutamate.
-1- PATHWAY: Peptidoglycan biosynthesis.
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-1- SIMILARITY: Belongs to the murCDB family.
-----
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CC -----
DR EMBL; AL935258; CAD64544.1; -.
DR HSSP; P14900; 2UAG.
DR HAMAP; MF_00639; -.
DR InterPro; IPR004101; Mur_ligase_C.
DR InterPro; IPR007113; Mur_ligase_N.
DR InterPro; IPR005762; MurD.
DR Pfam; PF01225; Mur_ligase_1.
DR Pfam; PF02875; Mur_ligase_C_1.
KW ATP-binding; Cell division; Cell wall; Complete proteome; Ligase;
KW Peptidoglycan synthesis.
FT NP_BIND 119 125 ATP (Potential).
FT SQ SEQUENCE 459 AA; 50137 MW; 083AB3E45C599DC9 CRC64;

Query Match 40.0%; Score 6; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 5 DNCETC 10
Db 75 DNCETC 80

RESULT 5
MURD LACPL STANDARD; PRT; 459 AA.
AC 088V80;
DT 28-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (UDP-N-
acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid
adding enzyme).
GN Name=Murd; OrderedLocusNames=lp_2197;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_Taxid=1590;

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QY 4 TDNCET 9
Db 403 TDNCET 408

RESULT 6
Q9C7H2 PRELIMINARY; PRT; 601 AA.
AC Q9C7H2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein F28P5.4 (Atlg72090/F28P5_4).
GN Name=F28P5.4;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosoids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
[1]
RP SEQUENCE FROM N.A.
RA Iln X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Matci R., Romling C.M., Koo H., Fujii C.Y., Utterback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.

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RA Shim P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN
RP
[3]
SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shim P., Bowser L., Carninci P.,
RA Chan M.W., Chang C.H., Dale J.M., Hayashizaki Y., Heuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC069273; AAG5137.1; -
DR EMBL; AF367274; AAK56263.1; -
DR EMBL; BT002712; AAO11628.1; -
DR PIR; B96744; B96744.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0005506; F: iron ion binding; IEA.
DR InterPro; IPR006638; E1p3/MiAB/NiFB.
DR InterPro; IPR006466; MiAB like B.
DR InterPro; IPR007197; Radical_SAM.
DR InterPro; IPR005839; UPF0004.
DR Pfam; PF04055; Radical_SAM; 1.
DR Pfam; PF01938; TRAM; 1.
DR Pfam; PF00919; UPF0004; 1.
DR SMART; SM00729; E1p3; 1.
DR TIGRFAMs; TIGR01578; MiAB-like-B; 1.
DR TIGRFAMs; TIGR00089; UPF0004; 1.
DR PROSITE; PS50926; TRAM; 1.
DR PROSITE; PS01278; UPF0004; 1.
DR KEGG; K01278; UPF0004; 1.
DR Hypothetical protein.
SQ
SEQUENCE 601 AA; 65496 MW; AAC13F7EFCB3DAD3 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CETCTC 12
DB 514 CETCTC 519

RESULT 7
ID O81A76 PRELIMINARY; PRT; 1068 AA.
AC O81A76;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform b.
GN Name=pl1-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Felodierinae; Caenorhabditis.
OC NCBI_TaxID=6239;
OX
ON
RN
RP
[1]
SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium. ";
RL Science 283:2012-2018 (1998).
RN
RP
[2]
SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
```

```
RA Wohldmann P., Beck C.;
RT "The sequence of C. elegans cosmid K10F12."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN
RP
[3]
SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN
RP
[4]
SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN
RP
[5]
SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RC Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN
RP
[6]
SEQUENCE FROM N.A.
RA STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1 - SIMILARITY: Contains 1 C2 domain.
DR EMBL; AF025462; AAN72423.1; -
DR HSSP; P10688; 1DJH.
DR WormBase; WBGene0004045; pl1-1.
DR WormPEP; K10F12.3b; CE31037.
DR GO; GO:0004435; F: phospholipase C activity; IEA.
DR GO; GO:0007242; F: intracellular signaling cascade; IEA.
DR GO; GO:0006629; P: lipid metabolism; IEA.
DR InterPro; IPR000088; C2.
DR InterPro; IPR008973; C2_CaLB.
DR InterPro; IPR001849; PH_related.
DR InterPro; IPR011036; PI_PLC.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_X.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC_X; 1.
DR Pfam; PF00387; PI_PLC_Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00148; PLCX; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2 DOMAIN 2; 1.
DR PROSITE; PS50004; C2 DOMAIN 1; 1.
DR PROSITE; PS50007; PI_PLC_X DOMAIN; 1.
DR PROSITE; PS50009; PI_PLC_Y DOMAIN; 1.
SQ
SEQUENCE 1068 AA; 120042 MW; 98F7CFCFFD7EC221 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 1068;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCET 9
DB 310 TDNCET 315

RESULT 8
ID O81A75 PRELIMINARY; PRT; 1075 AA.
AC O81A75;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform a.
GN Name=pl1-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
```

OC Rhabdittidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium.";
 RL Science 282:2012-2018 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wohldmann P., Beck C.;
 RT "The sequence of *C. elegans* cosmid K10F12.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 C2 domain.
 DR EMBL: AF025462; NANT2422.1; -.
 DR HSSP: P10688; IDH.
 DR WormBase; WBGene00004045; p11-1.
 DR WormPep; K10F12.3a; CE31036.
 DR GO: GO:0004435; F:phosphoinositide phospholipase C activity; IEA.
 DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO: GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR000008; C2.
 DR InterPro; IPR008973; C2_CaLB.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011036; PH-related.
 DR InterPro; IPR001192; PI_PLC.
 DR InterPro; IPR000909; PI_PLC_X.
 DR InterPro; IPR001711; PI_PLC_Y.
 DR Pfam; PF00168; C2; 1.
 DR Pfam; PF00388; PI_PLC-X; 1.
 DR Pfam; PF00387; PI_PLC-Y; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00390; PHPLIPASEC.
 DR ProDom; PD001202; PI_PLC_Y; 1.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00148; PLCYC; 1.
 DR SMART; SM00149; PLCYC; 1.
 DR PROSITE; PSS0004; C2 DOMAIN 2; 1.
 DR PROSITE; PSS0007; PIPLC_X DOMAIN; 1.
 DR PROSITE; PSS0008; PIPLC_Y DOMAIN; 1.
 SQ SEQUENCE 1075 AA; 12111 MW; 6102111ABF78AFD4 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 1075;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 TDNCET 9
 317 TDNCET 322

RESULT 9
 ID 070Z09 PRELIMINARY; PRT; 1615 AA.
 AC 070Z09;
 DT 01-MAR-2004 (TREMblrel. 26, Created)
 DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE GLP_609_15416_20263.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome.";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: ACB0100040; EAA40566.1; -.
 DR HSSP: P35555; IEMN.
 DR GO: GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR005127; Giardia VSP.
 DR InterPro; IPR009030; Grow fac. recept.
 DR InterPro; IPR002049; Laminin_EGF.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00053; Laminin_EGF; 1.
 DR Pfam; PF03302; VSP; 1.
 DR PROSITE; PS00022; EGF_1; 4.
 DR PROSITE; PS01186; EGF_2; 12.
 DR PROSITE; PSS0026; EGF_3; 2.
 DR PROSITE; PSS01248; LAMININ TYPE_EGF; 4.
 SQ SEQUENCE 1615 AA; 16955 MW; B86E3D60D18B4F27 CRC64;

Query Match 40.0%; Score 6; DB 2; Length 1615;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 DNCETC 10
 1261 DNCETC 1266

RESULT 10
 ID 070H34 PRELIMINARY; PRT; 1870 AA.
 AC 070H34;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE VAVV Bangladesh B22R orthologue.
 OS Name=fp9.122;
 GN Fowlpox virus (isolate HP-438 (Munich)).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OX NCBI_TaxID=10263;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Skinner M.A., Laidlaw S.M.;
 RT "Comparison of the genome sequence of FP9, an attenuated, tissue
 RT culture-adapted European fowlpox virus, with those of virulent
 RT American and European viruses.";
 RL J. Gen. Virol. 85:305-322 (2004).
 DR EMBL: AJ581527; CAE52663.1; -.
 DR InterPro; IPR007490; Poxvirus_B22R.
 DR Pfam; PF04395; Poxvirus_B22R; 1.
 SQ SEQUENCE 1870 AA; 211756 MW; 2423D319743D3F2F CRC64;

```

Query Match          40.0%; Score 6; DB 2; Length 1870;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 NCERTCT 11
      |||||
Db      241 NCERTCT 246

RESULT 11
Q9J5A0 PRELIMINARY; PRT; 1870 AA.
AC Q9J5A0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF FPV122 variola B22R gene family protein.
GN Name=FPV122;
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RX DOI=10.1126/JVT.74.8.3815-3831.2000;
RA Afonso C.L., Tuitman E.R., Lu Z., Zaak L., Kutish G.F., Rock D.L.;
RT "The genome of Fowlpox virus."
RL J. Virol. 74:3815-3831(2000).
DR EMBL; AF198100; AAF44466.1; -.
DR InterPro; IPR007490; Poxvirus_B22R.
DR Pfam; PF04395; Poxvirus_B22R; 1.
SQ SEQUENCE 1870 AA; 21156 MW; 2423D319743D3F2F CRC64;

Query Match          40.0%; Score 6; DB 2; Length 1870;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 NCERTCT 11
      |||||
Db      241 NCERTCT 246

RESULT 12
LMA2 HUMAN
ID LMA2_HUMAN STANDARD; PRT; 3110 AA.
AC P24043; Q14736; Q93022;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy
chain).
GN Name=LAMA2; Synonyms=LAMW;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=94124633; PubMed=8294519; DOI=10.1083/jcb.124.3.381;
RX Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
RX Hironen H., Showe T.B., Sariola H., Engvall E., Tryggvason K.;
RT "Human laminin M chain (merosin): complete primary structure,
RT chromosomal assignment, and expression of the M and A chain in human
RT fetal tissues."
RL J. Cell Biol. 124:381-394(1994).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97066955; PubMed=8910357; DOI=10.1074/jbc.271.44.27664;
RX Zhang X., Vuolteenaho R., Tryggvason K.;
RT "Structure of the human laminin alpha2-chain gene (LAMA2), which is

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RT affected in congenital muscular dystrophy."
RL J. Biol. Chem. 271:27664-27669(1996).
RN [3]
RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=90238994; PubMed=2185464;
RX Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E.;
RT "Merosin, a tissue-specific basement membrane protein, is a laminin-
RT like protein."
RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
RN [4]
RP VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
RA Marzluft G.A., Amato A.A., Mendell J.R.;
RT "Novel single base polymorphisms and rare sequence variants in the
RT laminin 2-chain coding region detected by RFLP/SSCP analysis."
RL Hum. Mutat. 13:174-174(1999).
RN [5]
RP ERRATUM.
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
RA Marzluft G.A., Amato A.A., Mendell J.R.;
RL Hum. Mutat. 13:340-340(1999).
RN [6]
RP VARIANTS MDCL1A PRO-2564.
RX MEDLINE=21476011; PubMed=11591858;
RX He Y., Jones K.J., Vignier N., Morgan G., Chevallay M., Barois A.,
RX Estournet-Mathiad B., Hori H., Mizuta T., Tome F.M.S., North K.N.,
RX Gulcheney P.;
RT "Congenital muscular dystrophy with primary partial laminin alpha-2
RT chain deficiency: molecular study."
RL Neurology 57:1319-1322(2001).
RN [7]
RP VARIANTS MDCL1A TYR-527 AND ARG-862.
RX MEDLINE=22439669; PubMed=12552556; DOI=10.1002/humu.10157;
RX Tezak Z., Prandini P., Boscaro M., Marin A., Devaney J., Marino M.,
RX Fanin M., Trevisan C.P., Park J., Tyson W., Finkel R., Garcia C.,
RX Angelini C., Hoffman E.P., Pegoraro E.;
RT "Clinical and molecular study in congenital muscular dystrophy with
RT partial laminin alpha-2 (LAMA2) deficiency."
RL Hum. Mutat. 21:103-111(2003).
RN [8]
RP FUNCTION: Binding to cells via a high affinity receptor, laminin
RN is thought to mediate the attachment, migration and organization
RN of cells into tissues during embryonic development by interacting
RN with other extracellular matrix components.
CC [9]
RP SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The alpha-2 chain is a subunit of laminin-2 (merosin) and
CC laminin-4 (5-merosin).
CC [10]
RP SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC [11]
RP TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve,
CC cardiac muscle, pancreas, lung, spleen, kidney, adrenal gland,
CC skin, testis, meninges, choroid plexus, and some other regions of
CC the brain; not in liver, thymus and bone.
CC [12]
RP DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC [13]
RP DOMAIN: Domains VI, IV and G are globular.
CC [14]
RP DISEASE: Defects in LAMA2 are the cause of merosin-deficient
CC congenital muscular dystrophy type 1A (MDCL1A) [MIM:607855]. MDCL1A
CC is characterized by difficulty walking, hypotonia, proximal
CC weakness, hyporeflexia, and white matter hypodensity on MRI.
CC [15]
RP SIMILARITY: Contains 17 laminin EGF-like domains.
CC [16]
RP SIMILARITY: Contains 5 laminin G-like domains.
CC [17]
RP SIMILARITY: Contains 2 laminin IV domains.
CC [18]
RP SIMILARITY: Contains 1 laminin N-terminal domain.
CC [19]
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DR EMBL; Z26553; CAAB1394.1; -
 DR EMBL; U66796; AAB18388.1; JOINED.
 DR EMBL; U66733; AAB18388.1; JOINED.
 DR EMBL; U66735; AAB18388.1; JOINED.
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 DR EMBL; U66743; AAB18388.1; JOINED.
 DR EMBL; U66745; AAB18388.1; JOINED.
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 DR EMBL; U66749; AAB18388.1; JOINED.
 DR EMBL; U66750; AAB18388.1; JOINED.
 DR EMBL; U66751; AAB18388.1; JOINED.
 DR EMBL; U66752; AAB18388.1; JOINED.
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 DR EMBL; U66754; AAB18388.1; JOINED.
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 DR EMBL; U66779; AAB18388.1; JOINED.
 DR EMBL; U66780; AAB18388.1; JOINED.
 DR EMBL; U66781; AAB18388.1; JOINED.
 DR EMBL; U66782; AAB18388.1; JOINED.
 DR EMBL; U66783; AAB18388.1; JOINED.
 DR EMBL; U66784; AAB18388.1; JOINED.
 DR EMBL; U66785; AAB18388.1; JOINED.
 DR EMBL; U66786; AAB18388.1; JOINED.
 DR EMBL; U66787; AAB18388.1; JOINED.
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 DR EMBL; U66789; AAB18388.1; JOINED.
 DR EMBL; U66790; AAB18388.1; JOINED.
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 DR EMBL; U66792; AAB18388.1; JOINED.
 DR EMBL; U66793; AAB18388.1; JOINED.
 DR EMBL; U66794; AAB18388.1; JOINED.
 DR EMBL; U66795; AAB18388.1; JOINED.
 DR EMBL; MS9832; AAA63215.1; -
 DR PIR; FX0082; MMTUHH.
 DR HSSP; Q60675; IDYK.
 DR Genew; HGNC; 6482; LAMA2.
 DR MIM; 607855; -
 DR GO; GO:0005604; C:Basement membrane; TMS.

DR GO; GO:0005198; F:structural molecule activity; TMS.
 DR GO; GO:0007517; P:muscle development; TMS.
 DR InterPro; IPR008985; Cona_like_1ec_g1.
 DR InterPro; IPR006203; BGF_like.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR000034; Laminin B.
 DR InterPro; IPR002049; Laminin EGF.
 DR InterPro; IPR001791; Laminin G.
 DR InterPro; IPR003254; Laminin I.
 DR InterPro; IPR010307; Laminin II.
 DR InterPro; IPR008211; Laminin N.
 DR InterPro; IPR003129; TSP N.
 DR Pfam; PF00052; Laminin B; 2.
 DR Pfam; PF00053; Laminin B; 14.
 DR Pfam; PF00054; Laminin G; 5.
 DR Pfam; PF06008; Laminin I; 1.
 DR Pfam; PF06009; Laminin II; 1.
 DR Pfam; PF00055; Laminin N; 1.
 DR PRINTS; PR00011; BGF/LAMININ.
 DR PRODOM; PD003031; Laminin B; 2.
 DR PROSITE; PS00022; EGF_1; 11.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50025; LAM G DOMAIN; 5.
 DR PROSITE; PS01248; LAMININ TYPE EGF; 14.
 KM Basement membrane; Cell adhesion; Coiled coil;
 KM Congenital muscular dystrophy; Direct protein sequencing;
 Query Match 40.0%; Score 6; DB 1; Length 3110;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 NCERTCT 11
 Db 389 NCERTCT 394
 RESULT 13
 ID DEFA_ANDAU STANDARD; PRT; 37 AA.
 AC P56686; P81618;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 4 kDa defensin.
 OS Androctonus australis (Sahara scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butrida; Butiridae; Butiridae; Androctonus.
 OX NCBI_TaxID=6858;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC STRAIN=Hector; TISSUE=Hemolymph;
 RX MEDLINE=97094646; PubMed=8939880; DOI=10.1074/jbc.271.47.29537;
 RA Ehret-Sabatie L., Loew D., Goyffon M., Fehlbauer P., Hoffmann J.A.,
 RA van Dorselaer A., Bulet P.;
 RT "Characterization of novel cysteine-rich antimicrobial peptides from
 RT scorpion blood.";
 RL J. Biol. Chem. 271:29537-29544(1996).
 CC -1- FUNCTION: Active against Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=4206.8; METHOD=Electrospray; RANGE=1-37;
 CC NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
 DR HSSP; P80571; IFUN.
 DR InterPro; IPR001542; Defensin_anpod.
 DR Pfam; PF01097; Defensin 2; 1.
 DR PROSITE; PS00425; ARTHROPOD DEFENSINS; 1.
 KM Antibiotic; Defensin; Direct protein sequencing.
 FT DISULFID 4 25 By similarity.
 FT DISULFID 11 33 By similarity.
 FT DISULFID 15 35 By similarity.
 SQ SEQUENCE 37 AA; 4212 MW; AB1363EC3FB84C1 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13
 |||||
 Db 32 TCTCY 36

RESULT 14
 DEF4_LEI0H STANDARD; PRT; 38 AA.
 AC P41965;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 4 kDa defensin (Antibacterial 4 kDa peptide).
 OS Leiurus quinquestriatus hebraeus (Yellow scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butridia; Butchoidea; Butridae; Leiurus.
 NCBI_TaxID=6884;
 OX NCBI_TaxID=6884;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=93326112; PubMed=8333834;
 RA Cocciandich S., Goyffon M., Bontems F., Bulet P., Bouet F., Menez A.,
 Hoffmann J.A.;
 RT "Purification and characterization of a scorpion defensin, a 4kDa
 RT antibacterial peptide presenting structural similarities with insect
 RT defensins and scorpion toxins.";
 RL Biochem. Biophys. Res. Commun. 194:17-22(1993).
 CC -1- FUNCTION: Antibacterial protein against Gram-positive bacteria;
 CC may act via membrane-permeabilization of these cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
 DR PIR, UN0613; UN0613.
 DR HSSP; P80571; IFUN.
 DR InterPro; IPR001542; Defensin_anpd.
 DR Pfam; PF01097; Defensin_2; 1.
 DR PROSITE; PS00425; ARTHROPOD DEFENSINS; 1.
 KW Antibiotic; Defensin; Direct protein sequencing.
 FT DISULFID 4 25 By similarity.
 FT DISULFID 11 33 By similarity.
 FT DISULFID 15 35 By similarity.
 SQ SEQUENCE 38 AA; 4326 MW; DF35FB21BCB3FB84 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13
 |||||
 Db 32 TCTCY 36

RESULT 15
 DEF1_AESCY STANDARD; PRT; 38 AA.
 AC P80154;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Defensin.
 OS Aeschna cyanea (Dragonfly) (Blue darner).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Palaeoptera; Odonata; Anisoptera; Aeshnidae; Aeshna.
 NCBI_TaxID=12921;
 OX NCBI_TaxID=12921;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=93049356; PubMed=1425705;
 RA Bulet P., Cocciandich S., Reuland M., Sauber F., Bischoff R., Hegy G.,
 van Dorsselaer A., Hetru C., Hoffmann J.A.;

RT "A novel insect defensin mediates the inducible antibacterial activity
 RT in larvae of the dragonfly Aeschna cyanea (Palaeoptera, Odonata).";
 RL Eur. J. Biochem. 209:977-984(1992).
 CC -1- FUNCTION: Mediates the inducible antibacterial activity in larvae
 CC of A. cyanea.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
 DR PIR, S27242; S27242.
 DR HSSP; P80571; IFUN.
 DR InterPro; IPR001542; Defensin_anpd.
 DR Pfam; PF01097; Defensin_2; 1.
 DR PROSITE; PS00425; ARTHROPOD DEFENSINS; 1.
 KW Antibiotic; Defensin; Direct protein sequencing; Insect immunity.
 FT DISULFID 4 26 By similarity.
 FT DISULFID 11 34 By similarity.
 FT DISULFID 15 36 By similarity.
 SQ SEQUENCE 38 AA; 4180 MW; 7C884A8DF54A46A CRC64;

Query Match 33.3%; Score 5; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13
 |||||
 Db 33 TCTCY 37

Search completed: May 4, 2005, 14:33:08
 Job time : 26.7455 secs

CC patients with a disease characterized by elevated levels of FSH. The

XX
SQ Sequence 64 AA;

Query Match 100.0%; Score 64; DB 5; Length 64;
Best Local Similarity 100.0%; Pred. No. 5, 6e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYETETISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
DB 1 EWQDNCETCTCYETETISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60

QY 61 EWII 64
DB 61 EWII 64

RESULT 2

AAO17911 standard; protein; 94 AA.

AAO17911;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSF;
beta-microseminoprotein; human seminal plasma inhibin; analogue;
prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
benign prostate hyperplasia; cytosstatic.

Homo sapiens.

WO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02353334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for
inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
gastrointestinal, breast, endometrial, and ovarian cancers.

Disclosure; Page 73; 185pp; English.

The present invention relates to analogues of the human prostate
secretory protein of 94 amino acids (PSP94, also known as prostatic
inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
microseminoprotein (beta-MSF)). The analogues are useful for inhibiting
growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal
cancer, breast cancer, endometrial, ovarian or other cancers of
epithelial secretion, or benign prostate hyperplasia and for treating
patients with a disease characterized by elevated levels of FSH. The
present sequence is the human PSP94 protein

Sequence 94 AA;

Query Match 100.0%; Score 64; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EWQDNCETCTCYETETISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
|||||

DB 31 EWQDNCETCTCYETETISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 90

QY 61 EWII 64
DB 91 EWII 94

RESULT 3

ABR56227 standard; protein; 94 AA.

ABR56227;

20-NOV-2003 (first entry)

Native Human prostate secretory protein-94 (PSP-94).

Human; cytosstatic; prostate secretory protein-94; PSP-94;
hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;
parathyroid hormone related peptide; PTHrP; skeletal metastasis.

Homo sapiens.

WO2003039576-A1.

15-MAY-2003.

08-NOV-2002; 2002WO-CA001737.

08-NOV-2001; 2001CA-02361736.

(PROC-) PROCYON BIOPHARMA INC.

Rabdan SA, Shukeir N, Panchal CJ, Newman C;

WPI; 2003-441476/41.

Use of prostate secretory protein-94 for treating hypercalcaemia of
malignancy and reducing skeletal metastasis arising from carcinomas,
prostate and breast cancers.

Disclosure; Page 35; 61pp; English.

The present invention relates to the use of prostate secretory protein-94
(PSP-94; the present sequence) for treating a patient suffering from
hypercalcaemia of malignancy. PSP-94 is useful for treating a patient
suffering from hypercalcaemia of malignancy arising from carcinomas,
prostate and breast cancer. The PSP-94 is also useful for reducing
parathyroid hormone related peptide (PTHrP) levels in a patient in need
and reducing the development of skeletal metastasis. The PSP-94 is also
used for the manufacture of a pharmaceutical composition for the
treatment of hypercalcaemia of malignancy and/or skeletal metastasis

Sequence 94 AA;

Query Match 100.0%; Score 64; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EWQDNCETCTCYETETISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
DB 31 EWQDNCETCTCYETETISCTLVSTPVGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 90

QY 61 EWII 64
DB 91 EWII 94

RESULT 4

AAO17912 standard; protein; 102 AA.

AAO17912;

```

XX 30-AUG-2002 (first entry)
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #1.
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytosolic.
XX Homo sapiens.
XX
XX MO200233090-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-CA001463.
XX
XX 16-OCT-2000; 2000CA-02321256.
XX
XX 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 73-74; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
XX microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
XX
XX Sequence 102 AA;
XX
XX Query Match 100.0%; Score 64; DB 5; Length 102;
XX Best Local Similarity 100.0%; Pred. No. 8,6e-61;
XX Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EWQDNCETCTCYETETISCTLVSTPYGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
XX 39 EWQDNCETCTCYETETISCTLVSTPYGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 98
XX
XX 61 EWII 64
XX 99 EWII 102
XX
XX RESULT 5
XX ABR56228
XX ID ABR56228 standard; protein; 102 AA.
XX
XX ABR56228;
XX
XX 20-NOV-2003 (first entry)
XX
XX Recombinate prostate secretory protein-94 (PSP-94).
XX
XX Cytostatic; prostate secretory protein-94; PSP-94;
XX hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;
XX parathyroid hormone related peptide; PTHrP; skeletal metastasis.
XX

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OS unidentified.
XX
XX MO2003039576-A1.
XX
XX 15-MAY-2003.
XX
XX 08-NOV-2002; 2002WO-CA001737.
XX
XX 08-NOV-2001; 2001CA-02361736.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Rabbani SA, Shukelir N, Panchal CJ, Newman C;
XX WPI; 2003-441476/41.
XX
XX Use of prostate secretory protein-94 for treating hypercalcaemia of
XX malignancy and reducing skeletal metastasis arising from carcinomas,
XX prostate and breast cancers.
XX
XX Disclosure; Page 35-36; 61pp; English.
XX
XX The present invention relates to the use of prostate secretory protein-94
XX (PSP-94; the present sequence) for treating a patient suffering from
XX hypercalcaemia of malignancy. PSP-94 is useful for treating a patient
XX suffering from hypercalcaemia of malignancy arising from carcinomas,
XX prostate and breast cancer. The PSP-94 is also useful for reducing
XX parathyroid hormone related peptide (PTHrP) levels in a patient in need
XX and reducing the development of skeletal metastasis. The PSP-94 is also
XX used for the manufacture of a pharmaceutical composition for the
XX treatment of hypercalcaemia of malignancy and/or skeletal metastasis
XX
XX Sequence 102 AA;
XX
XX Query Match 100.0%; Score 64; DB 7; Length 102;
XX Best Local Similarity 100.0%; Pred. No. 8,6e-61;
XX Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 EWQDNCETCTCYETETISCTLVSTPYGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
XX 39 EWQDNCETCTCYETETISCTLVSTPYGYDKNCQRIFFKEDCKYIVVEKKDPKKTCSVS 98
XX
XX 61 EWII 64
XX 99 EWII 102
XX
XX Db
XX
XX RESULT 6
XX AAG03726
XX ID AAG03726 standard; protein; 114 AA.
XX
XX AAG03726;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein, SEQ ID NO: 7807.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GBST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclet A, Giordano J;
XX

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XX DR WPI, 2000-500381/45.
XX DR N-PSDB; AAC03732.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT operating cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 13; SEQ ID NO 7807; 71pp + Sequence Listing; English.
XX XX
XX CC The present sequence is a polypeptide encoded by one of a large number of
XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated
XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT
XX CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX CC sequences derived from the 5' ends of mRNAs and even in those cases where
XX CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX CC are also used in diagnostic, forensic, gene therapy and chromosome
XX CC mapping procedures. They are used to obtain upstream regulatory sequences
XX CC and to design expression and secretion vectors
XX SQ Sequence 114 AA;

Query Match 100.0%; Score 64; DB 3; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.6e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCTCYETETISCTLVSTPGYDKNCORIFKKEDCKYIVVEKKDPKKTCSVS 60
Db 51 EMQDNCCTCTCYETETISCTLVSTPGYDKNCORIFKKEDCKYIVVEKKDPKKTCSVS 110
QY 61 EWII 64
Db 111 EWII 114

RESULT 7
AAU28067
ID AAU28067 standard; protein; 114 AA.
XX
XX AC AAU28067;
XX XX
XX DT 18-DEC-2001 (first entry)
XX XX
XX DE Novel human secretory protein, Seq ID No 236.
XX XX
XX KM Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX KM ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
XX KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
XX KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
XX KM gut protection; lung; liver fibrosis; immune deficiency; infection;
XX KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
XX KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
XX KM fertility; analgesic; pain; antigen.
XX OS Homo sapiens.
XX PN WO200166689-A2.
XX PD 13-SEP-2001.
XX PF 05-MAR-2001; 2001WO-US004942.
XX PR 07-MAR-2000; 2000US-00519705.
XX PR 19-MAY-2000; 2000US-00574454.
XX PR 17-JUN-2000; 2000US-00596193.
XX PR 14-JUL-2000; 2000US-00616847.
XX PR 19-SEP-2000; 2000US-00655363.
XX PR 20-OCT-2000; 2000US-00693267.

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XX PA (HYSE-) HYSEQ INC.
XX XX
XX PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
XX PI Zhao QA, Yang Y, Dmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX DR WPI, 2001-589934/66.
XX DR N-PSDB; AAS44967.
XX PT Novel polypeptides and nucleic acids obtained from cDNA libraries
XX PT prepared from various human tissues, for diagnosis and treatment of
XX PT cancer, neurological, inflammatory, and autoimmune disorders.
XX PS Example 3; SEQ ID NO 236; 107pp; English.
XX XX
XX CC The invention relates to novel isolated human secreted polypeptides (I)
XX CC and polynucleotides (II). (I) and (II) are useful for treating
XX CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
XX CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
XX CC involved in increasing haematopoiesis, stem cell survival, bone growth
XX CC and remodeling. (I), (II) and modulators of (II) are useful for
XX CC prophylaxis or treatment of one or more cancers. (II) is also useful for
XX CC creating transgenic animals useful for studying the in vivo activities of
XX CC the polypeptide as well as for studying modulators of the polypeptides.
XX CC (I) induces the proliferation of neural cells and regeneration of nerve
XX CC and brain tissue and is useful for the treatment of central and
XX CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
XX CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
XX CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
XX CC activity, regulation of haematopoiesis and is useful for treating myeloid
XX CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
XX CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
XX CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
XX CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,
XX CC or periodontal disease. Furthermore, (I) is also useful for gut
XX CC protection or regeneration and treatment of lung or liver fibrosis,
XX CC reperfusion injury in various tissues, various immune deficiencies and
XX CC disorders including severe combined immunodeficiency (SCID), bacterial or
XX CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
XX CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
XX CC reactions and conditions, such as asthma or other respiratory problems.
XX CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
XX CC fertility, metabolism, catbolism, anabolism, storage or elimination of
XX CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
XX CC analgesic effects or other pain reducing effects, immunoglobulin like
XX CC activity and can act as an antigen in a vaccine composition to raise an
XX CC immune response. AAU28020-AAU28395 represent novel human secreted protein
XX CC amino acid sequences of the invention
XX SQ Sequence 114 AA;

Query Match 100.0%; Score 64; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.6e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCTCYETETISCTLVSTPGYDKNCORIFKKEDCKYIVVEKKDPKKTCSVS 60
Db 51 EMQDNCCTCTCYETETISCTLVSTPGYDKNCORIFKKEDCKYIVVEKKDPKKTCSVS 110
QY 61 EWII 64
Db 111 EWII 114

RESULT 8
ABR54574
ID ABR54574 standard; protein; 114 AA.
XX
XX AC ABR54574;
XX XX
XX DT 28-AUG-2003 (first entry)
XX XX
XX DE Prostatic secretory protein SEQ ID 1003.

```

XX Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KM Immune response; prostate cancer.
XX Homo sapiens.
XX WO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitchen JL, Harlocker SL, Jiang Y, Henderson RA,
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvyck TS,
PI Carter D, Li SX, Wang A, Skelky YAM, Hepler WT, Hural U,
PI Mcneill PD, Houghton RL, Vinals Y De Bassolec, Foy TW, Watanabe Y,
PI Deng T;
XX WPI; 2003-167130/16.
XX
DR New prostate-specific proteins and genes, useful in gene therapy,
XX particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Claim 2; Page 666; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 114 AA;
XX
Query Match 100.0%; Score 64; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.6e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKNCORIFKKEDCKYIVVEKKDPKKTGSVS 60
DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKNCORIFKKEDCKYIVVEKKDPKKTGSVS 110
QY 61 EWII 64
DB 111 EWII 114
XX
RESULT 9
ADB75447
ID ADB75447 standard; protein; 114 AA.
XX
AC ADB75447;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker protein.
XX
KM Prostate; cancer; cytostatic; gene therapy; marker.
XX
OS Homo sapiens.
XX
PN WO2003009814-A2.
XX
PD 06-FEB-2003.
XX

PF 25-JUL-2002; 2002WO-US023913.
XX
XX 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
XX (MILL-) MILENNIUM PHARM INC.
XX
PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B,
PI Hoersh S, Kamatkar S, Wonsey AM, Glat K, Zhao X, Anderson D;
XX WPI; 2003-248033/24.
XX
DR New nucleic acid molecule, useful for diagnosing or treating prostate
XX cancer.
XX
PT New nucleic acid molecule, useful for diagnosing or treating prostate
XX cancer.
XX
PS Disclosure; SEQ ID NO 271; 99pp; English.
XX
XX The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 114 AA;
XX
Query Match 100.0%; Score 64; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.6e-61;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKNCORIFKKEDCKYIVVEKKDPKKTGSVS 60
DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKNCORIFKKEDCKYIVVEKKDPKKTGSVS 110
QY 61 EWII 64
DB 111 EWII 114
XX
RESULT 10
ADB14453
ID ADB14453 standard; protein; 114 AA.
XX
AC ADB14453;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostatic secretory protein (PSP).
XX
XX Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
KM cell therapy; vaccine; T-cell epitope;
KM class I major histocompatibility complex allele; MHC; prostate cancer;
KM tumour; antigen presenting cell.
XX
XX Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX

DR WPI; 2004-042945/04.
XX
PT New combination comprising cDNAs and proteins that are differentially
PT expressed in respiratory disorders, useful for diagnosing or treating
PT respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
PT diseases or asthma.
XX
PS Claim 14; SEQ ID NO 270; 343bp; English.
XX
CC The invention relates to cDNA sequences that are differentially expressed
CC in respiratory disorders or their complements or encoded proteins. The
CC cDNAs and proteins are useful for diagnosing, treating or monitoring
CC treatment of a subject with a respiratory disease including lung cancer,
CC chronic obstructive pulmonary diseases, emphysema or asthma. The protein
CC is also useful for screening molecules or compounds to identify at least
CC one ligand which specifically binds the protein. It is also useful for
CC preparing and purifying a polyclonal or monoclonal antibody. This
CC sequence corresponds to a protein of the invention.
XX
SQ Sequence 114 AA;
XX
Query Match 100.0%; Score 64; DB 8; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.6e-61; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 51 EWQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 110
QY 61 EWII 64
DB 111 EWII 114
XX
RESULT 14
ADJ75600
ID ADJ75600 standard; protein; 114 AA.
AC ADJ75600;
XX
DT 20-MAY-2004 (first entry)
XX
DE Marker gene related amino acid sequence SEQ ID NO:852.
XX
KM bronchial asthma; chronic obstructive pulmonary disease;
KM respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX gene therapy; marker.
XX
OS Homo sapiens.
XX
PN EP1394274-A2.
XX
PD 03-MAR-2004.
XX
PF 04-AUG-2003; 2003EP-00254857.
XX
PR 06-AUG-2002; 2002JP-00229312.
PR 20-MAR-2003; 2003JP-00077212.
XX
PA (GENO-) GENOX RES INC.
XX
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX WPI; 2004-193155/19.
XX
DR WPI; 2004-193155/19.
XX
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
PS Example 11; SEQ ID NO 852; 241bp; English.
XX
CC The present invention describes a method of testing for bronchial asthma

CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC whose expression levels decrease when respiratory epithelial cells are
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (1) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.
XX
SQ Sequence 114 AA;
XX
Query Match 100.0%; Score 64; DB 8; Length 114;
Best Local Similarity 100.0%; Pred. No. 9.6e-61; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 51 EWQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKEDCKYIVVEKKDPKKTCSVS 110
QY 61 EWII 64
DB 111 EWII 114
XX
RESULT 15
ADN05811
ID ADN05811 standard; protein; 114 AA.
AC ADN05811;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic protein sequence #1069.
XX
KM antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GRTH) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;
XX Wu TD;
XX WPI; 2004-305105/28.
XX
DR N-PSDB; ADN05810.

XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX
 PS Claim 9; SEQ ID NO 2205; 3069pp; English.
 XX
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX
 SQ Sequence 114 AA;

Query Match 100.0%; Score 64; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 9.6e-61;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOTDNCETCTCYETETISCTLVSTPVGVDKNCORIFKKEDCKYIVVEKKDPKKTCSVS 60
 DB 51 EMOTDNCETCTCYETETISCTLVSTPVGVDKNCORIFKKEDCKYIVVEKKDPKKTCSVS 110

QY 61 EWII 64
 DB 111 EWII 114

Search completed: May 4, 2005, 14:25:10
 Job time: 130.396 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:13:33 ; Search time 32.8145 Seconds
(without alignments)
145.592 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 64

Sequence: 1 EMQDNCETCTCYETBISCC.....YIVVEKKPKKCSVSEMI 64

Scoring table: OLIGO

Searched: 513545 seqs, 74649064 residues

Word size: 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents AA:*
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5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	94	US-07-899-535A-1	Sequence 1, Appli
2	64	100.0	114	US-09-513-999C-7807	Sequence 7807, Ap
3	26	40.6	28	US-07-899-535A-4	Sequence 4, Appli
4	7	10.9	10	US-07-899-535A-2	Sequence 2, Appli
5	7	10.9	626	US-09-485-717-2	Sequence 2, Appli
6	7	10.9	626	US-09-948-722-2	Sequence 2, Appli
7	6	9.4	40	US-09-065-383-30	Sequence 30, Appli
8	6	9.4	66	US-09-270-767-39485	Sequence 39485, A
9	6	9.4	66	US-09-270-767-54702	Sequence 54702, A
10	6	9.4	104	US-08-858-207A-428	Sequence 428, App
11	6	9.4	114	US-08-252-991A-25178	Sequence 25178, A
12	6	9.4	165	US-09-902-540-15519	Sequence 15519, A
13	6	9.4	222	US-09-384-162-8	Sequence 8, Appli
14	6	9.4	241	US-08-460-309-17	Sequence 17, Appli
15	6	9.4	241	US-08-125-077-17	Sequence 17, Appli
16	6	9.4	265	US-09-543-681A-6305	Sequence 6305, Ap
17	6	9.4	338	US-09-270-767-46028	Sequence 46028, A
18	6	9.4	339	US-09-248-796A-16100	Sequence 16100, A
19	6	9.4	350	US-09-270-767-43557	Sequence 43557, A
20	6	9.4	363	US-09-328-352-5693	Sequence 5693, Ap
21	6	9.4	371	US-09-270-767-43550	Sequence 43550, A
22	6	9.4	393	US-08-888-429A-21	Sequence 21, Appli
23	6	9.4	393	US-09-593-653-21	Sequence 21, Appli
24	6	9.4	425	US-09-634-955B-19	Sequence 19, Appli
25	6	9.4	453	US-09-328-352-4181	Sequence 36, Appli
26	6	9.4	481	US-09-914-259-36	Sequence 35, Appli
27	6	9.4	486	US-09-914-259-35	Sequence 35, Appli

28	6	9.4	486	US-09-976-594-278	Sequence 278, App
29	6	9.4	486	US-09-949-016-6216	Sequence 6216, Ap
30	6	9.4	487	US-09-206-166-6	Sequence 6, Appli
31	6	9.4	489	US-09-328-352-5330	Sequence 5330, Ap
32	6	9.4	498	US-09-232-468A-18	Sequence 18, Appli
33	6	9.4	498	US-09-232-468A-24	Sequence 24, Appli
34	6	9.4	498	US-08-686-968C-231	Sequence 231, App
35	6	9.4	498	US-09-784-984B-52	Sequence 52, Appli
36	6	9.4	498	US-09-784-984B-54	Sequence 54, Appli
37	6	9.4	507	US-09-949-016-9878	Sequence 9878, Ap
38	6	9.4	512	US-07-779-890-4	Sequence 4, Appli
39	6	9.4	512	US-07-779-890-4	Sequence 4, Appli
40	6	9.4	512	US-09-008-962-4	Sequence 4, Appli
41	6	9.4	512	US-08-675-507-4	Sequence 4, Appli
42	6	9.4	512	US-09-213-205-4	Sequence 4, Appli
43	6	9.4	512	PCT-US93-05640-4	Sequence 4, Appli
44	6	9.4	518	US-09-065-383-27	Sequence 27, Appli
45	6	9.4	533	US-09-489-039A-7511	Sequence 7511, Ap

ALIGNMENTS

RESULT 1
US-07-899-535A-1
Sequence 1, Application US/07899535A

Patent No. 5428011

GENERAL INFORMATION:

APPLICANT: Sheth, Anil R.

APPLICANT: Panchal, Chandra J.

TITLE OF INVENTION: Pharmaceutical Preparations For

TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS: Adenocarcinoma, Stomach Cancer and Breast Cancer.

ADDRESS: Mr. George Loud

STREET: 2001 Jefferson Davis Highway, Suite 306

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/899,535A

FILING DATE: 16-JUN-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Loud, George A.

REGISTRATION NUMBER: 25,814

REFERENCE/DOCKET NUMBER: S&B-A835

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-0960

TELEFAX: 703-415-0962

TELEX: 24 8614

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 94 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

US-07-899-535A-1

Query Match 100.0%; Score 64; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.3e-62;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EMQMDNCECTICVETETETISCCCLVSTPVGYDKNDQRIFFKEDCKYIVAEKDPKTCVS	60
Db	31	EMQMDNCECTICVETETISCCCLVSTPVGYDKNDQRIFFKEDCKYIVAEKDPKTCVS	90
QY	61	EMII 64	
Db	91	EMII 94	

RESULT 2
US-09-513-999C-7807

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Sequence /807/, Application US/0951399C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J. Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
Patent No. 6783961
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513. 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36661
SOFTWARE: Patent.pm
SEQ ID NO 7807
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -20...-1
OTHER INFORMATION: score 9
IS-09-513-999C-7807
VFATFTVTLNNA/SC

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Best Local Similarity	100.0%	Pred. No. 1,5e-62		
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Db	51	EMQTNCECTCTCYETEISQCTLVSPVQYDQNCORIFKEDCKYIVWEKDPKTCVS	110	
Qy	61	EWII 64		
Db	111	EWII 114		

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RESULT 3
US-07-899-535A-4
; Sequence 4, Application US/07899535A
; Patent No. 5428011
;
; GENERAL INFORMATION:
;
; APPLICANT: Sheth, Anil R.
;
; APPLICANT: Garde, Seema
;
; TITLE OF INVENTION: Panchal, Chandra J.
;
; TITLE OF INVENTION: Pharmaceutical Preparations For
;
; TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
;
; TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer
;
; NUMBER OF SEQUENCES: 4
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Mr. George Loud
;
; STREET: 2001 Jefferson Davis Highway, Suite 306
;
; CITY: Arlington
;
; STATE: Virginia
;
; COUNTRY: U.S.A.
;
; ZIP: 22202
;
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS

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1  SOFTWARE: Patent in Release #1.0, Version #1.25
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/07/899,535A
4  FILING DATE: 16-JUN-1992
5  CLASSIFICATION: 514
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Loud, George A.
8  REGISTRATION NUMBER: 25,814
9  REFERENCE/DOCKET NUMBER: S&B-A835
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: 703-415-0960
12 TELEFAX: 703-415-0962
13
14 TELEX: 24 8614
15
16 INFORMATION FOR SEQ ID NO: 4:
17
18 SEQUENCE CHARACTERISTICS:
19
20 LENGTH: 28 amino acids
21
22 TYPE: amino acid
23
24 TOPOLOGY: linear
25
26 MOLECULE TYPE: peptide
27
28 HYPOTHEetical: NO
29
30 US-07-899-535A-4

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QY      37  IFFKEDCKYIVKKDPKTKCSVSEW 62
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Best Local Similarity 100.0%; Prod. No. 1.7e-21;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
 US-07-899-535A-2
 Sequence 2, Application US/07899535A
 Patent No. 5428011
 GENERAL INFORMATION:
 APPLICANT: Sheeh, Anil R.
 APPLICANT: Garde, Seema
 TITLE OF INVENTION: Panchal, Chandra J.
 TITLE OF INVENTION: Pharmaceutical Preparations For
 TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
 NUMBER OF INVENTIONS: Adenocarcinoma, Stomach Cancer and Breast Cancer
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Mr. George Loud
 STREET: 2001 Jefferson Davis Highway, Suite 306
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/899,535A
 FILING DATE: 16-JUN-1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Loud, George A.
 REGISTRATION NUMBER: 25,814
 REFERENCE/DOCKET NUMBER: SEB-A835
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-415-0960
 TELEFAX: 703-415-0962
 TELEX: 24 8614
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

HYPOTHETICAL: NO
US-07-899-535A-2

Query Match 10.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 TCYSVSEW 62
| | | | |
Db 2 TCYSVSEW 8

RESULT 5

US-09-485-717-2
; Sequence 2, Application US/09485717
; Patent No. 6673353
; GENERAL INFORMATION:
; APPLICANT: Kauffmann, Stefan
; APPLICANT: Hees, Jergen
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 16862PUS
; CURRENT APPLICATION NUMBER: US/09/485,717
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: EP 97114614.7
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: PCT/EP98-05109
; PRIOR FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant
US-09-485-717-2

Query Match 10.9%; Score 7; DB 4; Length 626;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIWEKK 51
| | | | |
Db 143 YIWEKK 149

RESULT 6

US-09-948-722-2
; Sequence 2, Application US/09948722
; Patent No. 6776993
; GENERAL INFORMATION:
; APPLICANT: Kauffmann, Stefan H. E.
; APPLICANT: Hees, Jergen
; TITLE OF INVENTION: Tuberculosis Vaccine
; FILE REFERENCE: 100564-00079
; CURRENT APPLICATION NUMBER: US/09/948,722
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/485,717
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PCT/EP98/05109
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: EP 97/114,614.7
; PRIOR FILING DATE: 1997-08-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 626
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: recombinant nucleic acid
; OTHER INFORMATION: molecule comprising a domain of Mycobacterium and a phagolysosomal
; OTHER INFORMATION: escape domain

US-09-948-722-2

Query Match 10.9%; Score 7; DB 4; Length 626;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIWEKK 51
| | | | |
Db 143 YIWEKK 149

RESULT 7

US-09-065-383-30
; Sequence 30, Application US/09065383
; Patent No. 6391543
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLETTIS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GORDON, JULIAN
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: HODGES, STEVEN C.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: KRATOCHVIL, JON D.
; APPLICANT: ROBERTS-RAP, LISA
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STROUPE, STEPHEN D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,383
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/842,385
; FILING DATE: 23-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6084.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6391543e
US-09-065-383-30

Query Match 9.4%; Score 6; DB 3; Length 40;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 VEKKDP 53
| | | | |

Db 4 VEKKDP 9

RESULT 8

US-09-270-767-39485
; Sequence 39485, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 39485

; LENGTH: 66

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-39485

Query Match 9.4%; Score 6; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 41 EDCKYI 46
Db 24 EDCKYI 29

RESULT 9

US-09-270-767-54702
; Sequence 54702, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 54702

; LENGTH: 66

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-54702

Query Match 9.4%; Score 6; DB 4; Length 66;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 41 EDCKYI 46
Db 24 EDCKYI 29

RESULT 10

US-08-858-207A-428
; Sequence 428, Application US/08858207A
; Patent No. 6348328

; GENERAL INFORMATION:

; APPLICANT: Black, Michael

; APPLICANT: Hodgson, John

; APPLICANT: Knowles, David

; APPLICANT: Nicholas, Richard

; APPLICANT: Stodola, Robert

; TITLE OF INVENTION: No 6348328e1 Compounds

; NUMBER OF SEQUENCES: 552

CORRESPONDENCE ADDRESS:

ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/858,207A

FILING DATE: 09-MAY-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/017670

FILING DATE: 14-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Gimmil, Howard R

REGISTRATION NUMBER: 38,891

REFERENCE/DOCKET NUMBER: P50475

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-4478

TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 428:

SEQUENCE CHARACTERISTICS:

LENGTH: 104 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6348328e

US-08-858-207A-428

Query Match 9.4%; Score 6; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 27 VGYDKD 32
Db 47 VGYDKD 52

RESULT 11

US-09-252-991A-25178
; Sequence 25178, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 25178

; LENGTH: 114

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-25178

Query Match 9.4%; Score 6; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 TLVSTP 26

Db 65 TLVSTP 70

RESULT 12
US-09-902-540-15519
Sequence 15519, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(115849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 15519
LENGTH: 165
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-15519

Query Match 9.4%; Score 6; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 VSTPVG 28
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Db 86 VSTPVG 91

RESULT 13
US-09-384-162-8
Sequence 8, Application US/09384162
Patent No. 6376747
GENERAL INFORMATION:
APPLICANT: Xing, Ti
APPLICANT: Malik, Kamal
APPLICANT: Martin-Heller, Teresa
APPLICANT: Miki L., Brian
TITLE OF INVENTION: No. 6376747el Plant-Derived Map Kinase Kinase
FILE REFERENCE: 08-884280US
CURRENT APPLICATION NUMBER: US/09/384,162
CURRENT FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 222
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-384-162-8

Query Match 9.4%; Score 6; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 DCKYIV 47
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Db 56 DCKYIV 61

RESULT 14
US-08-460-309-17
Sequence 17, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leiyo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof

NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-17

Query Match 9.4%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
|||||
Db 103 NCERTCT 108

RESULT 15
US-08-125-077-17
Sequence 17, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leiyo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ. ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-17

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Query Match          9.4%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 NCETCT 11
Db      103 NCETCT 108

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Search completed: May 4, 2005, 14:37:22
Job time : 33.8145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:33:36 ; Search time 71.4473 Seconds

(without alignments)
298.385 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 64
Sequence: 1 EMQDNCETCTCYETETISCC.....YIVVEKKDKPKTCSVSEWII 64

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Searched: 1426032 seqs, 333106140 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:*

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19: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*

20: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	64	100.0	94	10	US-09-977-406A-1
3	64	100.0	94	14	US-10-291-360-1
4	64	100.0	94	17	US-10-857-358-1
5	64	100.0	102	10	US-09-977-406A-2
6	64	100.0	102	14	US-10-291-360-2
7	64	100.0	102	17	US-10-857-358-2
8	64	100.0	114	13	US-10-012-896-1003
9	64	100.0	114	14	US-10-203-823-271
10	64	100.0	114	14	US-10-144-678A-1003
11	64	100.0	114	14	US-10-294-025-1003
12	64	100.0	114	15	US-10-291-172-236
13	64	100.0	114	15	US-10-221-278-236

14	64	100.0	114	16	US-10-408-765A-532	Sequence 532, App
15	64	100.0	132	9	US-09-925-300-1027	Sequence 1027, App
16	64	98.4	63	10	US-09-977-406A-57	Sequence 57, App
17	62	96.9	62	10	US-09-977-406A-56	Sequence 56, App
18	61	95.3	60	10	US-09-977-406A-55	Sequence 55, App
19	60	93.8	60	10	US-09-977-406A-54	Sequence 54, App
20	59	92.2	59	10	US-09-977-406A-53	Sequence 53, App
21	58	90.6	58	10	US-09-977-406A-52	Sequence 52, App
22	57	89.1	57	10	US-09-977-406A-51	Sequence 51, App
23	56	87.5	56	10	US-09-977-406A-50	Sequence 50, App
24	55	85.9	55	10	US-09-977-406A-49	Sequence 49, App
25	54	84.4	54	10	US-09-977-406A-48	Sequence 48, App
26	53	82.8	53	10	US-09-977-406A-47	Sequence 47, App
27	52	81.2	52	10	US-09-977-406A-46	Sequence 46, App
28	51	79.7	51	10	US-09-977-406A-45	Sequence 45, App
29	50	78.1	50	10	US-09-977-406A-44	Sequence 44, App
30	49	76.6	49	10	US-09-977-406A-43	Sequence 43, App
31	48	75.0	48	10	US-09-977-406A-42	Sequence 42, App
32	47	73.4	47	10	US-09-977-406A-41	Sequence 41, App
33	46	71.9	46	10	US-09-977-406A-40	Sequence 40, App
34	45	70.3	45	10	US-09-977-406A-39	Sequence 39, App
35	44	68.8	44	10	US-09-977-406A-38	Sequence 38, App
36	43	67.2	43	10	US-09-977-406A-37	Sequence 37, App
37	42	65.6	42	10	US-09-977-406A-36	Sequence 36, App
38	41	64.1	41	10	US-09-977-406A-35	Sequence 35, App
39	40	62.5	40	10	US-09-977-406A-34	Sequence 34, App
40	39	60.9	39	10	US-09-977-406A-33	Sequence 33, App
41	38	59.4	38	10	US-09-977-406A-32	Sequence 32, App
42	37	57.8	37	10	US-09-977-406A-31	Sequence 31, App
43	36	56.2	36	10	US-09-977-406A-30	Sequence 30, App
44	35	54.7	35	10	US-09-977-406A-29	Sequence 29, App
45	34	53.1	34	10	US-09-977-406A-28	Sequence 28, App

ALIGNMENTS

RESULT 1

US-09-977-406A-58

Sequence 58, Application US/09977406A

Publication No. US20030170220A1

GENERAL INFORMATION:

APPLICANT: PROCOYON BIOPHARMA INC.

TITLE OR INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS

FILE REFERENCE: 06508-030-US-03

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: US/09/977,406A

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 58

LENGTH: 64

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Polypeptide derived from rHUPSP4 sequence (polypeptide analog)

US-09-977-406A-58

Query Match 100.0%; Score 64; DB 10; Length 64;

Best Local Similarity 100.0%; Pred. No. 1e-59;

Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCCITVSTPGYDKDKORIFKEDCKYIVVEKKDKPKTCSVS 60

DB 1 EMQDNCETCTCYETETISCCITVSTPGYDKDKORIFKEDCKYIVVEKKDKPKTCSVS 60

QY 61 EWII 64

DB 61 EWII 64

RESULT 2
US-09-977-406A-1
Sequence 1, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Ulvback, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and
AUTHORS: Lundwall, A.
TITLE: Molecular cloning of a small prostate protein, known as beta-
TITLE: microsemenoprotein, PSP94 or beta-inhibin, and demonstration of transcripts
TITLE: non-genital tissues.
JOURNAL: Biochem. Biophys. Res Commun.
VOLUME: 164
ISSUE: 3
PAGES: 1310-1315
DATE: 1989
DATABASE ACCESSION NUMBER: GI 131436
DATABASE ENTRY DATE: 1988-08-01
US-09-977-406A-1

Query Match 100.0%; Score 64; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTIVSTPVGYDKNQCRIFKEDCKYIVVEKDPKKTCSVS 60
DB 31 EMQDNCETCTCYETETISCTIVSTPVGYDKNQCRIFKEDCKYIVVEKDPKKTCSVS 90

QY 61 EWII 64
DB 91 EWII 94

RESULT 3
US-10-291-360-1
Sequence 1, Application US/10291360
Publication No. US20030119744A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-051-US-02
CURRENT APPLICATION NUMBER: US/10/291,360
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Ulvback, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and
AUTHORS: Lundwall, A.
TITLE: Molecular cloning of a small prostate protein, known as beta-
TITLE: microsemenoprotein, PSP94 or beta-inhibin, and demonstration of transcripts
TITLE: non-genital tissues.

JOURNAL: Biochem. Biophys. Res Commun.
VOLUME: 164
ISSUE: 3
PAGES: 1310-1315
DATE: 1989
DATABASE ACCESSION NUMBER: GI 131436
DATABASE ENTRY DATE: 1988-08-01
US-10-291-360-1

Query Match 100.0%; Score 64; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTIVSTPVGYDKNQCRIFKEDCKYIVVEKDPKKTCSVS 60
DB 31 EMQDNCETCTCYETETISCTIVSTPVGYDKNQCRIFKEDCKYIVVEKDPKKTCSVS 90

QY 61 EWII 64
DB 91 EWII 94

RESULT 4
US-10-857-358-1
Sequence 1, Application US/10857358
Publication No. US20050026633A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-153
CURRENT APPLICATION NUMBER: US/10/857,358
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 10/291,360
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Ulvback, M., Lindstrom, C., Weiber, H., Abrahamson, P.A., Lilja, H., and
AUTHORS: Lundwall, A.
TITLE: Molecular cloning of a small prostate protein, known as beta-
TITLE: microsemenoprotein, PSP94 or beta-inhibin, and demonstration of transcripts
TITLE: non-genital tissues.
JOURNAL: Biochem. Biophys. Res Commun.
VOLUME: 164
ISSUE: 3
PAGES: 1310-1315
DATE: 1989
DATABASE ACCESSION NUMBER: GI 131436
DATABASE ENTRY DATE: 1988-08-01
US-10-857-358-1

Query Match 100.0%; Score 64; DB 17; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.5e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTIVSTPVGYDKNQCRIFKEDCKYIVVEKDPKKTCSVS 60
DB 31 EMQDNCETCTCYETETISCTIVSTPVGYDKNQCRIFKEDCKYIVVEKDPKKTCSVS 90

QY 61 EWII 64
DB 91 EWII 94

RESULT 5
US-09-977-406A-2
Sequence 2, Application US/09977406A

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; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant human PSP94 (rHuPSP94) produced from yeast
US-09-977-406A-2

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Query Match      100.0%; Score 64; DB 10; Length 102;
Best Local Similarity 100.0%; Pred. No. 1,6e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EMOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 60
DB      39 EMOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 98
QY      61 EWII 64
DB      99 EWII 102

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RESULT 6
US-10-291-360-2
; Sequence 2, Application US/10291360
; Publication No. US20030119744A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
; FILE REFERENCE: 06508-051-US-02
; CURRENT APPLICATION NUMBER: US/10/291,360
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: CA 2,361,736
; PRIOR FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant human PSP94 (rHuPSP94) produced from yeast
US-10-291-360-2

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Query Match      100.0%; Score 64; DB 14; Length 102;
Best Local Similarity 100.0%; Pred. No. 1,6e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EMOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 60
DB      39 EMOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 98
QY      61 EWII 64
DB      99 EWII 102

```

```

RESULT 7
US-10-857-358-2
; Sequence 2, Application US/10857358
; Publication No. US20050026833A1

```

```

; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
; FILE REFERENCE: 06508-153
; CURRENT APPLICATION NUMBER: US/10/857,358
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: CA 2,361,736
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 10/291,360
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant human PSP94 (rHuPSP94) produced from yeast
US-10-857-358-2

```

```

Query Match      100.0%; Score 64; DB 17; Length 102;
Best Local Similarity 100.0%; Pred. No. 1,6e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EMOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 60
DB      39 EMOTDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKKTCSVS 98
QY      61 EWII 64
DB      99 EWII 102

```

```

RESULT 8
US-10-012-896-1003
; Sequence 1003, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hurral, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Panger, Gary R.
; APPLICANT: Mantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1003
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-10-012-896-1003

Query Match
Best Local Similarity 100.0%; Score 64; DB 13; Length 114;
Pred. No. 1.7e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKTKCSVS 60
DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKTKCSVS 110
QY 61 EWTI 64
DB 111 EWTI 114

RESULT 9

US-10-205-823-271
Sequence 271, Application US/10205823
Publication No. US20030108963A1

GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbacheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamackar, Shubhangt
APPLICANT: Monsey, Angela M.
APPLICANT: Glatz, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205, 823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307, 982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314, 356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325, 020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341, 746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362, 158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 271
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-271

Query Match
Best Local Similarity 100.0%; Score 64; DB 14; Length 114;
Pred. No. 1.7e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKTKCSVS 60
DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKTKCSVS 110
QY 61 EWTI 64
DB 111 EWTI 114

RESULT 10

US-10-144-678A-1003
Sequence 1003, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa W.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144, 678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1003
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-1003

Query Match
Best Local Similarity 100.0%; Score 64; DB 14; Length 114;
Pred. No. 1.7e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKTKCSVS 60
DB 51 EMQDNCETCTCYETETISCTLVSTPVGYDKDNCORIFKKEDCKYIVVEKKDPKTKCSVS 110
QY 61 EWTI 64
DB 111 EWTI 114

RESULT 11

US-10-294-025-1003
Sequence 1003, Application US/10294025
Publication No. US20030185830A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294, 025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1003
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-025-1003

Query Match
Best Local Similarity 100.0%; Score 64; DB 14; Length 114;
Pred. No. 1.7e-59;

Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
 DB 51 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110
 QY 61 EWII 64
 DB 111 EWII 114

RESULT 12
 US-10-291-172-236
 ; Sequence 236, Application US/10291172
 ; Publication No. US20030228584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-045
 ; CURRENT APPLICATION NUMBER: US/10/291,172
 ; CURRENT FILING DATE: 2000-11-08
 ; PRIOR APPLICATION NUMBER: 09/693,267
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/665,363
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 09/616,847
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 09/596,193
 ; PRIOR FILING DATE: 2000-06-17
 ; PRIOR APPLICATION NUMBER: 09/574,454
 ; PRIOR FILING DATE: 2000-05-19
 ; PRIOR APPLICATION NUMBER: 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; NUMBER OF SEQ ID NOS: 752
 ; SEQ ID NO 236
 ; LENGTH: 114
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-291-172-236

Query Match 100.0%; Score 64; DB 15; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.7e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
 DB 51 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110
 QY 61 EWII 64
 DB 111 EWII 114

RESULT 13
 US-10-221-278-236
 ; Sequence 236, Application US/10221278
 ; Publication No. US20040034208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 21272-045
 ; CURRENT APPLICATION NUMBER: US/10/221,278
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: 09/693,267
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 09/665,363
 ; PRIOR FILING DATE: 2000-09-19
 ; PRIOR APPLICATION NUMBER: 09/616,847
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 09/596,193
 ; PRIOR FILING DATE: 2000-06-17
 ; PRIOR APPLICATION NUMBER: 09/574,454
 ; PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705
 ; PRIOR FILING DATE: 2000-03-07
 ; NUMBER OF SEQ ID NOS: 752
 ; SEQ ID NO 236
 ; LENGTH: 114
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-221-278-236

Query Match 100.0%; Score 64; DB 15; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.7e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
 DB 51 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110
 QY 61 EWII 64
 DB 111 EWII 114

RESULT 14
 US-10-408-765A-532
 ; Sequence 532, Application US/10408765A
 ; Publication No. US20040101874A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Fahy, Bojn D.
 ; APPLICANT: Zhang, Bing
 ; APPLICANT: Gibson, Bradford W.
 ; APPLICANT: Taylor, Steven W.
 ; APPLICANT: Glenn, Gary M.
 ; APPLICANT: Warnock, Dale E.
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
 ; FILE REFERENCE: 66088,465
 ; CURRENT APPLICATION NUMBER: US/10/408,765A
 ; CURRENT FILING DATE: 2003-04-04
 ; NUMBER OF SEQ ID NOS: 307
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 532
 ; LENGTH: 114
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-408-765A-532

Query Match 100.0%; Score 64; DB 16; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.7e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 60
 DB 51 EMOTDNCCTCTCYETETISCTLVSTPVGDKDNCQRIFFKEDCKYIVVEKKDPKKTCSVS 110
 QY 61 EWII 64
 DB 111 EWII 114

RESULT 15
 US-09-925-300-1027
 ; Sequence 1027, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05988
 ; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 1027
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-925-300-1027

Query Match 100.0%; Score 64; DB 9; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2e-59;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EMOTDNCETCTCYETETISCTIVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKTCVS	60
Db	69	EMOTDNCETCTCYETETISCTIVSTPVGYDKDNCQRIFFKEDCKYIVVEKDPKTCVS	60
QY	61	EWII	64
Db	129	EWII	132

Search completed: May 4, 2005, 15:24:07
 Job time : 71.4473 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:12:38 ; Search time 23.04 Seconds
(without alignments)
267.269 Million cell updates/sec

Title: US-09-977-406A-58

Perfect score: 64
Sequence: 1 EMQJNCETCTCCTETBISCC.....YIVVEKKDPKKTCSVSEWII 64Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	100.0	114	2	A34567
2	18	28.1	114	2	A54663
3	2	10.9	91	2	S41663
4	7	10.9	113	2	PC1244
5	7	10.9	113	2	S26482
6	7	10.9	528	2	S22341
7	7	10.9	529	2	S24231
8	7	10.9	529	2	A43505
9	7	10.9	529	2	AC1100
10	7	10.9	530	2	S22340
11	7	10.9	917	2	T22898
12	6	9.4	129	2	B80228
13	6	9.4	132	1	PKRT1
14	6	9.4	132	2	T03397
15	6	9.4	137	2	T33245
16	6	9.4	146	2	P82418
17	6	9.4	150	2	H64576
18	6	9.4	151	2	E71051
19	6	9.4	153	2	S48970
20	6	9.4	159	2	F83858
21	6	9.4	203	2	G97380
22	6	9.4	203	2	AF2598
23	6	9.4	208	2	T33326
24	6	9.4	266	2	B82713
25	6	9.4	278	2	S64317
26	6	9.4	285	2	H69369
27	6	9.4	288	2	A70371
28	6	9.4	304	2	AH1240
29	6	9.4	304	2	AD1603

30	6	9.4	311	1	BYEBT	sulfate-binding pr
31	6	9.4	319	2	T46145	hypothetical prote
32	6	9.4	324	2	T24465	hypothetical prote
33	6	9.4	326	2	JC7094	nine-heme cytochr
34	6	9.4	328	2	H71871	hypothetical prote
35	6	9.4	333	2	B82924	hypothetical prote
36	6	9.4	337	2	C71875	hypothetical prote
37	6	9.4	343	1	DEBYMP	malate dehydrogena
38	6	9.4	356	2	T19715	hypothetical prote
39	6	9.4	377	2	T32798	hypothetical prote
40	6	9.4	379	2	A88066	protein R52.3 (imp
41	6	9.4	384	2	T38544	probable exopolyp
42	6	9.4	406	2	T24492	hypothetical prote
43	6	9.4	425	2	C64516	hypothetical prote
44	6	9.4	430	2	C64554	ATP-dependent nucl
45	6	9.4	437	2	H84865	probable sterol de

ALIGNMENTS

RESULT 1
A34567
beta-microseminoprotein precursor - human
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pro
C:Species: Homo sapiens (man)
C:Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 09-Jul-2004
C:Accession: A34567; A26451; A29777; A30964; A60673; S16238; I52882
R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein ge
A:Reference number: A34567; MUID:90211299; PMID:2322265
A:Accession: A34567
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-114 <GRE>
A:Cross-references: UNIPROT:P08118; GB:M34376; NID:G514370; PID:AAA59871.1; PID:G514372
R:Mbakay, M.; Nole, S.; Fournier, S.; Benjannet, S.; Chapelaine, P.; Paradies, G.; Dube
DNA 6, 23-29, 1987
A:Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma p
A:Reference number: A26451; MUID:87161231; PMID:3829888
A:Accession: A26451
A:Molecule type: mRNA
A:Residues: 1-114 <MBI>
A:Cross-references: GB:M15885; NID:G338414; PID:AAA36635.1; PID:G338415
R:Akiyama, K.; Yoshioke, Y.; Schmidt, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara, M
Biochim. Biophys. Acta 829, 288-294, 1985
A:Title: The amino acid sequence of human beta-microseminoprotein.
A:Reference number: A29777; MUID:85199974; PMID:3995056
A:Accession: A29777
A:Molecule type: Protein
A:Residues: 21-58, 'PT', 61-113 <AKI>
R:Seidah, N.G.; Arabaci, N.J.; Rochement, J.; Sheth, A.R.; Chretien, M.
PNAS Lett. 175, 349-355, 1984
A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction of
A:Reference number: A30964; MUID:85004133; PMID:6434350
A:Accession: A30964
A:Molecule type: Protein
A:Residues: 21-112, 'G', 114 <SEI>
R:Weber, H.; Andersson, C.; Murne, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
Am. J. Pathol. 137, 593-604, 1990
A:Title: Beta microseminoprotein is not a prostate-specific protein.
A:Reference number: A60673; MUID:90379237; PMID:2205099
A:Accession: A60673
A:Molecule type: Protein
A:Residues: 21, 'X', 23-34 <WEI>
A:Experimental source: Gastric juice
R:Nollet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16238
A:Molecule type: DNA

Db 70 PKKTCV 76

RESULT 6

S22341
Ivanolysin precursor - *Listeria ivanovii*
C/Species: *Listeria ivanovii*
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C/Accession: S22341, S36683
R/Haas, A.; Dumbsky, M.; Kreft, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A/Title: *Listeria* monocytogenes: complete sequence of ilo from *Listeria ivanovii* and of lac
A/Reference number: S22340; MUID:92182018; PMID:1543752
A/Accession type: DNA
A/Residues: 1-528 <HAS>
A/Cross-references: UNIPROT:P13183; EMBL:X60461
A/Note: the authors translated the codon ACA for residue 331 as Val
R/Kreft, J.
submitted to the EMBL Data Library, July 1991
A/Reference number: S36683
A/Accession: S36683
A/Molecule type: DNA
A/Residues: 1-319, 'T', 321-528 <KRB>
A/Cross-references: EMBL:X60461
C/Genetics:
A/Status: preliminary
A/Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R/Mengaud, J.; Chenevert, J.; Geoffroy, C.; Gaillard, J.L.; Coesart, P.
Infect. Immun. 55, 3225-3227, 1987
A/Title: Identification of the structural gene encoding the SH-activated hemolysin of *Li*
F/1-24/Domain: *Ivanolysin* #status predicted <MAT>
F/25-528/Product: *Ivanolysin* #status predicted <MAT>

Query Match 10.9%; Score 7; DB 2; Length 528;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51

Db 97 YIVVEKK 103

RESULT 7

S24231
Listeria precursor - *Listeria monocytogenes* (strain 12067)
C/Species: *Listeria monocytogenes*
A/Variety: strain 12067
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S24231
R/Rasmussen, O.F.; Beck, T.; Olsen, J.E.; Dons, L.; Rosse, L.
Infect. Immun. 59, 3945-3951, 1991
A/Title: *Listeria monocytogenes* isolates can be classified into two major types according
A/Reference number: S24230; MUID:92040062; PMID:1937753
A/Accession: S24231
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-529 <RAS>
A/Cross-references: UNIPROT:P13128; EMBL:X60035; NID:944110; PIDN:CAA42639.1; PID:G44112
A/Experimental source: strain 12067, serotype 4b
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991
C/Genetics:
A/Gene: *lisa*
C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-529/Product: *Ivanolysin* #status predicted <MAT>

Query Match 10.9%; Score 7; DB 2; Length 529;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51

Db 98 YIVVEKK 104

RESULT 8

A43505
Listeria O precursor - *Listeria monocytogenes*
C/Species: *Listeria monocytogenes*
C/Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 09-Jul-2004
C/Accession: A43505, S05306, A47606; S12400; A61079
R/Mengaud, J.; Vicente, M.P.; Chenevert, J.; Pereira, J.M.; Geoffroy, C.; Gicquel-Sanzey, I.
Infect. Immun. 56, 766-772, 1988
A/Title: Expression in *Escherichia coli* and sequence analysis of the *Ivanolysin* O de
A/Reference number: A43505; MUID:88153053; PMID:3126142
A/Accession: A43505
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-529 <MEN>
A/Cross-references: UNIPROT:P13128; GB:M24199; NID:944106; PIDN:CAA33223.1; PID:G44107
A/Note: this sequence is derived from a strongly hemolytic strain, serotype 1/2c
R/Domann, E.; Chakraborty, T.
Nucleic Acids Res. 17, 6406, 1989
A/Title: Nucleotide sequence of the *Ivanolysin* gene from a *Listeria monocytogenes* ser
A/Reference number: S05306; MUID:89366684; PMID:2505236
A/Accession: S05306
A/Molecule type: DNA
A/Residues: 1-529 <DOM>
A/Cross-references: EMBL:X15127; NID:944106; PIDN:CAA33223.1; PID:G44107
A/Experimental source: strain EGD
A/Note: this sequence is derived from a weakly hemolytic strain, serotype 1/2a
R/Mengaud, J.; Chenevert, J.; Geoffroy, C.; Gaillard, J.L.; Coesart, P.
Infect. Immun. 55, 3225-3227, 1987
A/Title: Identification of the structural gene encoding the SH-activated hemolysin of *Li*
A/Reference number: A47606; MUID:88057627; PMID:2824384
A/Accession: A47606
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 413-480 <ME2>
A/Cross-references: GB:M29171
R/Michel, E.; Reich, K.A.; Favier, R.; Berche, P.; Coesart, P.
Mol. Microbiol. 4, 2167-2178, 1990
A/Title: Attenuated mutants of the intracellular bacterium *Listeria monocytogenes* obtain
A/Reference number: S12400; MUID:91211627; PMID:1965218
A/Accession: S12400
A/Molecule type: DNA
A/Residues: 483-493 <MIC>
A/Experimental source: strain LO28, serotype 1/2c
C/Genetics:
A/Gene: *hlyA*, *lisa*
C/Superfamily: dipeptide transport protein
C/Keywords: virulence factor
F/1-25/Domain: signal sequence #status predicted <SIG>
F/26-529/Product: *Ivanolysin* O #status predicted <MAT>

Query Match 10.9%; Score 7; DB 2; Length 529;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51

Db 98 YIVVEKK 104

RESULT 9

AC1100
Ivanolysin O precursor [imported] - *Listeria monocytogenes* (strain EGD-e)
C/Species: *Listeria monocytogenes*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C/Accession: AC1100
R/Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Feigl, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuzpakt, G.; Madueno, E.; Maltournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of *Listeria* species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1100
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-529 <GLA>
A:Cross-references: UNIPROT:P13128; GB:NC_003210; PIDN:CAD00729.1; PID:g16409567; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: hly
C:Superfamily: dipeptide transport protein

Query Match 10.9%; Score 7; DB 2; Length 529;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51
|||||
DB 98 YIVVEKK 104

RESULT 10
S22340
seeligeriolysin - *Listeria seeligeri*
C:Species: *Listeria seeligeri*
C>Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C:Accession: S22340
R:Haas, A.; Dumbeky, M.; Kreft, J.
Biochim. Biophys. Acta 1130, 81-84, 1992
A:Title: *Listeriolysin* genes: complete sequence of *llo* from *Listeria ivanovii* and of *lsc*
A:Reference number: S22340; MUID:92182018; PMID:1543752
A:Accession: S22340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <HAA>
A:Cross-references: UNIPROT:P31830; EMBL:X60462; NID:g44144; PIDN:CAA42996.1; PID:g44145
A:Note: the authors translated the codon GCC for residue 287 as Pro
C:Superfamily: dipeptide transport protein

Query Match 10.9%; Score 7; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVEKK 51
|||||
DB 99 YIVVEKK 105

RESULT 11
T22898
hypothetical protein F58B3.5 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22898
R:Harris, B.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z19633
A:Accession: T22898
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-917 <MTL>
A:Cross-references: UNIPROT:Q20970; EMBL:Z73427; PIDN:CAA97803.1; GSPDB:GN00022; CESP:FS
A:Experimental source: clone F58B3
C:Genetics:
A:Gene: CESP:F58B3.5
A:Map position: 4
A:introns: 27/2, 135/2, 620/1, 655/1, 874/3
C:Superfamily: methionyl-tRNA synthetase, dimer-forming

Query Match 10.9%; Score 7; DB 2; Length 917;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 VEKKDPK 54

DB 20 VEKKDPK 26
|||||
RESULT 12
B90228
hypothetical protein SS00783 [imported] - *Sulfolobus solfataricus*
C:Species: *Sulfolobus solfataricus*
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: B90228
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Chan-Y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: *Sulfolobus solfataricus* complete genome.
A:Reference number: A91139
A:Accession: B90228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <KUR>
A:Cross-references: UNIPROT:Q9UXH0; GB:AE006641; NID:g13813959; PIDN:AAK41081.1; GSPDB:G
A:Gene: SS00783

Query Match 9.4%; Score 6; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 IVEKK 51
|||||
DB 121 IVEKK 126

RESULT 13
F2RT1
fatty acid-binding protein, intestinal - rat
N:Alternate names: FABP
C:Species: *Rattus norvegicus* (Norway rat)
C>Date: 17-Dec-1982 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I65761; A03147
R:Gordon, J.I.; Lowe, J.B.
Chem. Phys. Lipids 38, 137-158, 1985
A:Title: Analyzing the structures, functions and evolution of two abundant gastrointestinal
A:Reference number: I52850; MUID:86053743; PMID:3840724
A:Accession: I65761
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-132 <RES>
A:Cross-references: UNIPROT:P02693; GB:M35992; NID:g204087; PIDN:AAA41141.1; PID:g204088
R:Alpers, D.H.; Strauss, A.W.; Ockner, R.K.; Baes, N.M.; Gordon, J.I.
Proc. Natl. Acad. Sci. U.S.A. 81, 313-317, 1984
A:Title: Cloning of a cDNA encoding rat intestinal fatty acid binding protein.
A:Reference number: A03147; MUID:84119477; PMID:6582489
A:Accession: A03147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-9, 'Y', 11-82, 'L', 84-132 <ALP>
A:Cross-references: GB:X01180; NID:g204081; PIDN:AAA41138.1; PID:g204082
C:Superfamily: myelin p2 protein
C:Keywords: blocked amino end; intestine; lipid binding
F12/Modified site: blocked amino end (Ala) (in mature form) (probably acetylated) #status
F12/Binding site: fatty acid (Arg) #status predicted

Query Match 9.4%; Score 6; DB 1; Length 132;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 RIFKKE 41
|||||
DB 127 RIFKKE 132

RESULT 14
T03397

hypothetical protein - maize (fragment)
C/Species: Zea mays (maize)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C/Accession: T03397
R/Alba, M.M.; Vinti, G.; Messegue, R.; Pages, M.
submitted to the EMBL Data Library, April 1997
A/Reference number: Z14927
A/Accession: T03397
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-132 <Alb>
A/Cross-references: UNIPROT:O04169; EMBL:X12762; NID:e1045993; PIDN:CAA73301.1; PID:e314
A/Experimental source: strain L.W64-A

Query March 9.4%; Score 6; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 VSTRPVG 28
|||||
Db 101 VSTRPVG 106

RESULT 15

T43245
probable actin-depolymerizing factor - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43245; T38120
R/Kawamukai, M.
submitted to the EMBL Data Library, December 1996
A/Description: S. pombe cDNA for actin depolymerizing factor.
A/Reference number: Z22362
A/Accession: T43245
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-137 <KAW>
A/Cross-references: UNIPROT:P78929; EMBL:D89939; PIDN:BAU14039.1
R/Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1996
A/Reference number: Z21771
A/Accession: T38120
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-137 <CON>
A/Cross-references: EMBL:Z98600; PIDN:CAB1258.1; GSPDB:GN00066; SPDB:SPAC20G4.06c
A/Experimental source: strain 972h-; cosmid c20G4
C/Genetics:
A/Gene: SPAC20G4.06c
A/Map position: 1
A/Introns: 1/3; 37/1
A/Note: adf1
C/Superfamily: cofilin
C/Keywords: actin binding

Query March 9.4%; Score 6; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 IVEEKK 51
|||||
Db 39 IVEEKK 44

Search completed: May 4, 2005, 14:34:55
Job time : 25.04 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:04:27 ; Search time 109.847 Seconds

(without alignments)
298.351 Million cell updates/sec

Title: US-09-977-406a-58

Perfect score: 64
Sequence: 1 EMQDNCETCTCYETETISCC.....YIVVEKKDPKKTCSVSEMI 64

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	114	1 MSMB_HUMAN	P08118 homo sapien
2	18	28.1	114	1 MSMB_MACMU	P25142 macaca mula
3	15	23.4	114	1 MSPJ_SAGOE	O97949 saguinus oe
4	13	20.3	112	1 MSPA_SAGOE	O97936 saguinus oe
5	9	14.1	114	1 MSMB_PAPAN	Q28767 papio anubi
6	9	14.1	114	1 MSPB_SAGOE	O97935 saguinus oe
7	8	12.5	366	2 O891V1	O891v1 clostridium
8	8	12.5	391	2 O6DDP3	O6ddp3 xenopus lae
9	8	12.5	416	2 O6NTV1	O6ntv1 xenopus lae
10	7	10.9	111	1 MSMB_PIG	O02826 sus scrofa
11	7	10.9	113	1 CGHR_XANMA	P31125 xanthomonas
12	7	10.9	141	2 O7P7S4	O7p7s4 fusobacteri
13	7	10.9	143	2 O83TZ3	O83tz3 listeria mo
14	7	10.9	143	2 O83U86	O83u86 listeria mo
15	7	10.9	143	2 O840A3	O840a3 listeria mo
16	7	10.9	143	2 O840A4	O840a4 listeria mo
17	7	10.9	288	2 O9VH00	O9vho0 drosophila
18	7	10.9	406	2 O6HK46	O6hka6 bacillus th
19	7	10.9	438	2 O6FWU4	O6fwu4 candida gla
20	7	10.9	525	2 O6R6D0	O6r6d0 listeria iv
21	7	10.9	528	1 TACY_LISIV	P18131 listeria iv
22	7	10.9	528	1 O6R6D9	O6r6d9 listeria iv
23	7	10.9	529	1 TACY_LISMF	Q72411 listeria mo
24	7	10.9	529	1 TACY_LISMO	P31128 listeria mo
25	7	10.9	529	2 O6E9T2	O6e9t2 listeria mo
26	7	10.9	529	2 O6E9A2	O6e9a2 listeria mo
27	7	10.9	529	2 O6E9G2	O6e9g2 listeria mo
28	7	10.9	529	2 O6E9Q2	O6e9q2 listeria mo
29	7	10.9	529	2 O6E9T2	O6e9t2 listeria mo
30	7	10.9	529	2 O6EA28	O6ea28 listeria mo
31	7	10.9	529	2 O6EA46	O6ea46 listeria mo

ALIGNMENTS

RESULT 1	ID	MSMB_HUMAN	STANDARD	PRT	114 AA.
AD	P08118	P11999	Q13125	Q9UC59	
DT	01-AUG-1988	(Rel. 08, Created)			
DT	01-AUG-1988	(Rel. 08, Last sequence update)			
DT	05-JUN-2004	(Rel. 44, Last annotation update)			
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PM44).				
DE	Name=MSMB; Synonyms=PRSP;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=87161231; PubMed=382988;				
RA	Molikay M., Nolet S., Pournier S., Benjannet S., Chapelaine P.,				
RA	Paradis G., Dube J.Y., Tremblay R., Lazare C., Seidan N.G.,				
RA	Chretien M.;				
RT	"Molecular cloning and sequence of the cDNA for a 94-amino-acid				
RT	seminal plasma protein secreted by the human prostate.";				
RT	DNA 6:23-29(1987).				
RL	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=91274357; PubMed=2054385; DOI=10.1016/0167-4781(91)90016-F;				
RA	Nolet S., Molikay M., Chretien M.;				
RT	"Prostatic secretory protein PSP94: gene organization and promoter				
RT	sequence in rhesus monkey and human.";				
RT	Biochim. Biophys. Acta 1089:247-249(1991).				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=90211299; PubMed=2322265;				
RA	Green C.B., Liu W.Y., Kwok S.C.M.;				
RT	"Cloning and nucleotide sequence analysis of the human beta-				
RT	microseminoprotein gene.";				
RT	Biochem. Biophys. Res. Commun. 167:1184-1190(1990).				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=90073664; PubMed=2590204;				
RA	Ulvbeck M., Lindstrom C., Welber H., Abrahamsson P.-A., Lilja H.,				
RA	Lundvall A.;				
RT	"Molecular cloning of a small prostate protein, known as beta-				
RT	microseminoprotein, PSP94 or beta-inhibin, and demonstration of				
RT	transcripts in non-genital tissues.";				
RT	Biochem. Biophys. Res. Commun. 164:1310-1315(1989).				
RL	[5]				
RP	SEQUENCE FROM N.A.				
RP	TISUS=Prostate;				
RC	MEDLINE=94115955; PubMed=7506990; DOI=10.1016/0304-3835(93)90049-F;				
RA	Liu A.Y., Bradner R.C., Vessella R.L.;				
RT	"Decreased expression of prostatic secretory protein PSP94 in prostate				
RT	cancer.";				

32	7	10.9	529	2	O6EAB7	O6eab7 listeria mo
33	7	10.9	529	2	O6EAB0	O6eab0 listeria mo
34	7	10.9	529	2	O6EAB4	O6eab4 listeria mo
35	7	10.9	529	2	O9LSB9	O9lsb9 listeria mo
36	7	10.9	530	1	TACY_LISSE	P18130 listeria se
37	7	10.9	756	2	O7Q8V8	O7q8v8 anopheles g
38	7	10.9	801	2	O6MGP8	O6mgp8 bdellovibri
39	7	10.9	848	2	O9AYE2	O9aye2 oryza sativ
40	7	10.9	861	2	O750Z5	O750z5 ashbya gos
41	7	10.9	917	1	STM_CAEBL	Q20970 caenorhabdi
42	7	10.9	1083	2	O6W5B5	O6w5b5 brachydanio
43	7	10.9	1378	2	O9LTA4	O9lta4 arabidopsis
44	7	10.9	2587	2	O6IMT0	O6imto arabidopsis
45	6	9.4	30	2	O86818	O86818 influenza a


```

FT      VASPUBLIC      78      114      Missing (in isoform PSP5).
                                           /FTID=VSP_003276.

Query Match      100.0%; Score 64; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 8,96-62;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1      EMOTDNCCTCYEFETISCTLVSPVGYDNDNCORIFKEDCKYIVEXKDPKTCVS 60
Db      51      EMOTDNCCTCYEFETISCTLVSPVGYDNDNCORIFKEDCKYIVEXKDPKTCVS 110
OY      61      EWII 64
           |||
           111      EWII 114

RESULT 2
MSMB_MACMU      STANDARD;      PRT;      114 AA.
ID      MSMB_MACMU
AC      P25142;
DT      01-MAY-1992 (Rel. 22, Created)
DT      01-MAY-1992 (Rel. 22, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Beta-microseminoprotein precursor (Prostate secreted seminal plasma
protein) (Prostate secretory protein PSP94) (PSP-94).
GN      Name=MSMB;
OS      Macaca mulatta (Rhesus macaque).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC      Cercopitheciinae; Macaca.
OX      NCBI_TaxID=9544;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=91274357; PubMed=2054385; DOI=10.1016/0167-4781(91)90016-F;
RA      Nolef S., Mblakay M., Chretien M.;
RT      "Prostatic secretory protein PSP94: gene organization and promoter
sequence in rhesus monkey and human."
RL      Biochim. Biophys. Acta 1089:247-249(1991).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91244325; PubMed=2037304;
RA      Nolef S., St Louis D., Mblakay M., Chretien M.;
RT      "Rapid evolution of prostatic protein PSP94 suggested by sequence
divergence between rhesus monkey and human cDNAs."
RL      Genomics 9:775-777(1991).
CC      -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC      -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; X57932; CAA41003.1; -.
DR      EMBL; X57933; CAA41003.1; JOINED.
DR      EMBL; X57934; CAA41003.1; JOINED.
DR      EMBL; X57935; CAA41003.1; JOINED.
DR      EMBL; M92161; AAA36903.1; -.
DR      PIR; S16237; A54663.
DR      InterPro; IPR009041; PMP_SGCI.
DR      InterPro; IPR008735; PSP94.
DR      Pfam; PF05825; PSP94; 1.
KM      Signal.
FT      SIGNAL      1      20      By similarity.
FT      CHAIN      21      114      Beta-microseminoprotein.
FT      DISULFID      22      38      By similarity.
FT      DISULFID      57      93      By similarity.
FT      DISULFID      60      69      Or C-60 with C-70 (By similarity).
FT      DISULFID      62      70      Or C-62 with C-69 (By similarity).

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FT DISULFID 84 107 By similarity
SQ SEQUENCE 114 AA; 13079 MW; C07A4EB984B276C CXC64;

Query Match 28.1%; Score 18; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CORIFKEDCKRIVEKK 51
DB 84 CORIFKEDCKRIVEKK 101

RESULT 3
MSPJ_SAGOE STANDARD; PRT; 114 AA.
ID MSPJ_SAGOE
AC 097949;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein J1 precursor (msp-J1).
OS Name=MSPJ;
SN Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginuss.
OX NCBI_TaxId=9490;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein.";
RT Eur. J. Biochem. 264:407-414(1999).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL; AJ010155; CAB38123.1; -.
DR EMBL; AJ010156; CAB38123.1; JOINED.
DR EMBL; AJ010157; CAB38123.1; JOINED.
DR GO; GO:0005576; C:extracellular; NAS.
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 114 Beta-microseminoprotein J1.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.
FT DISULFID 60 69 Or C-62 with C-70 (By similarity).
FT DISULFID 62 70 Or C-60 with C-69 (By similarity).
FT DISULFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 12746 MW; F3F05BD013445BAD4 CRC64;

Query Match 23.4%; Score 15; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 EISCTLVSTPVGYD 30
DB 66 EISCTLVSTPVGYD 80

RESULT 4
MSPA_SAGOE STANDARD; PRT; 112 AA.
ID MSPA_SAGOE
AC 097936;
DT 28-FEB-2003 (Rel. 41, Created)

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DT 28-FEB-2003 (Rel. 41, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Beta-microseminoprotein A1 precursor (msp-A1) (Fragment).
GN Name=MSRP;
OS Saginus oedipus (cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OC NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RT Eur. J. Biochem. 264:407-414(1999).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
CC EMBL; AJ010158; CAB38124.1; -.
CC GO; GO:0005576; C:extracellular; TMS.
CC InterPro; IPR002400; GP_CysKnot.
CC InterPro; IPR008735; PSP94.
CC Pfam; PF05825; PSP94; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC Signal.
FT NON TER 1 1
FT SIGNAL <1 19 By similarity.
FT CHAIN 20 112 Beta-microseminoprotein A1.
FT DISULFID 21 37 By similarity.
FT DISULFID 56 92 By similarity.
FT DISULFID 59 68 Or C-59 with C-69 (By similarity).
FT DISULFID 61 69 Or C-61 with C-68 (By similarity).
FT DISULFID 83 106 By similarity.
SQ SEQUENCE 112 AA; 12631 MW; D0A06BFC1C5CD78B CRC64;

Query Match 20.3%; Score 13; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 EDCRYIVVERKDP 53
DB 90 EDCRYIVVERKDP 102

RESULT 5
MSMB_PAPAN STANDARD; PRT; 114 AA.
AC Q28767;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
DE protein) (Prostate secretory protein PSP94) (PSP-94).
GN Name=MSMB; Synonyms=PSP94;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OC NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Prostate; PubMed=9174167;
RX MEDLINE=97316893; PubMed=9174167;
RX Pfam; PF05825; PSP94; 1.
RX Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Molikay M., Zhong R.,

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RA Chin J.L.;
RT "Molecular cloning and gene expression analysis of PSP94 (prostate
RT secretory protein of 94 amino acids) in primates."
RT DNA Cell Biol. 16:627-638(1997).
RL -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
CC EMBL; U49786; AAB62726.1; -.
CC InterPro; IPR008735; PSP94.
CC Pfam; PF05825; PSP94; 1.
CC Signal.
FT CHAIN 1 20 By similarity.
FT SIGNAL 21 114 Beta-microseminoprotein.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.
FT DISULFID 60 69 Or C-60 with C-70 (By similarity).
FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT DISULFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98ED CRC64;

Query Match 14.1%; Score 9; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 CKYIVVERK 51
DB 93 CKYIVVERK 101

RESULT 6
MSPE_SAGOE STANDARD; PRT; 114 AA.
AC Q97935;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein E1 precursor (msp-E1).
GN Name=MSPE;
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OC NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RX Maekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
RT beta-microseminoprotein."
RT Eur. J. Biochem. 264:407-414(1999).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ010154; CAB38105.1; -.
CC GO; GO:0005576; C:extracellular; TMS.
CC InterPro; IPR008735; PSP94.
CC Pfam; PF05825; PSP94; 1.
CC Signal.

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FT SIGNAL 1 20 Potential.
 FT CHAIN 21 114 Beta-microseminoprotein E1.
 FT DISULFID 22 38 By similarity.
 FT DISULFID 57 93 By similarity.
 FT DISULFID 60 69 Or C-60 with C-70 (By similarity).
 FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
 FT DISULFID 84 107 By similarity.
 SQ SEQUENCE 114 AA; 12738 MW; 05E7A410125C94B2 CRC64;
 Query Match 14.1%; Score 9; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.098;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 LVSTPVGVD 30
 DB 72 LVSTPVGVD 80
 RESULT 7
 ID 0891V1 PRELIMINARY; PRT; 368 AA.
 AC 0891V1;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Glycosyl transferase (EC 2.4.1.-).
 GN OrderedLocustNames=CTC02262;
 OS Clostridium tetrani.
 OC Clostridium.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_Taxid=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Massachusetts / E88;
 RX MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
 RA Brueggemann H., Baumeister S., Fricke W.F., Wietze A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetrani, the causative agent of
 RT tetanus disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
 DR EMBL; AE015943; AAC036744.1; -.
 DR GO; GO:0016577; P:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 368 AA; 42864 MW; E1143720ED1EB7A1 CRC64;
 Query Match 12.5%; Score 8; DB 2; Length 368;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 KKEDECKYI 46
 DB 209 KKEDECKYI 216
 RESULT 8
 ID 06DDF3 PRELIMINARY; PRT; 391 AA.
 AC 06DDF3;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE MGC81516 protein.
 GN Name=MGC81516;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocytes;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocytes;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshilyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.T., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocytes;
 RA Klein S., Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 DR EMBL; BC077617; AAH7617.1; -.
 DR GO; GO:0000452; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4_1.
 DR SMART; SM00184; RING_1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 391 AA; 44161 MW; 86AC09825D5DC6BC CRC64;
 Query Match 12.5%; Score 8; DB 2; Length 391;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 CTIVSTPV 27
 DB 253 CTIVSTPV 260
 RESULT 9
 ID 06NTV1 PRELIMINARY; PRT; 416 AA.
 AC 06NTV1;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MGC81516 protein.
 GN Name=MGC81516;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]

RT "Partial nucleotide sequence of the Xanthomonas maltophilia chorionic gonadotropin-like receptor.";
 RT Biochem. Biophys. Res. Commun. 190:371-376(1993).
 CC -1- CAUTION: Was originally (Ref.1) reported to be highly similar to the mammalian choriongonadotropin hormone receptor, but is not significantly related.
 CC -----
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 CC -----
 DR EMBL, X68371, CAA46451.1; -;
 DR PIR, S26482; S26482.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 113 AA; 12451 MW; 5746ACE575FB61C2 CRC64;

Query Match 10.9%; Score 7; DB 1; Length 113;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 PKKTCV 59
 DB 70 PKKTCV 76

RESULT 12

07P7S4 PRELIMINARY; PRT; 141 AA.
 AC 07P7S4;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DE Methionyl-trna formyltransferase (EC 2.1.2.9).
 GN Name=MNV1719;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteriales; Fusobacteriaceae;
 CC Fusobacterium.
 CC NCBI_Taxid=209882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49256;
 RA Karpalraj V., Ivanova N., Anderson I., Reznik G., Bhattacharya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyripides N.;
 RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RL -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
 CC EMBL; AABF01000010; EAA24942.1; -;
 CC HSSP; P23882; 1FMT.
 DR GO: GO:0004479; F:methionyl-trna formyltransferase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0009058; P:biocynthesis; IEA.
 DR InterPro; IPR01034; FMT_C like.
 DR InterPro; IPR002376; Formyl_transfer_N.
 KM Transferase.
 SQ SEQUENCE 141 AA; 15874 MW; 035FBC96F5538772 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 141;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 FKXEDCK 44
 DB 34 FKXEDCK 40

RESULT 13

083TZ3 PRELIMINARY; PRT; 143 AA.
 AC 083TZ3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DE Listeriolysin O (Fragment).
 GN Name=hlyA;
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 CC NCBI_Taxid=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CECT 911, CECT 938, CTC 1010, CTC 1011, CECT 4031, and CECT 932.
 RX PubMed=1506755; DOI=10.1128/AEM.70.3.1366-1377.2004.
 RA Rodriguez-Lazaro D., Hernandez M., Scotti M., Beteve T., Vazquez-Boland J.A., Pla M.;
 RT "Quantitative Detection of Listeria monocytogenes and Listeria innocua by Real-time PCR: Assessment of hly, iap, and lln02483 Targets and AmpliFluor Technology.";
 RT Appl. Environ. Microbiol. 70:1366-1377(2004).
 RL Appl. Environ. Microbiol. 70:1366-1377(2004).
 DR EMBL; AY174657; AAO46015.1; -;
 DR EMBL; AY174663; AAO46021.1; -;
 DR EMBL; AY174665; AAO46023.1; -;
 DR EMBL; AY174668; AAO46026.1; -;
 DR EMBL; AY174668; AAO46024.1; -;
 DR HSSP; P19995; 1M31.
 DR GO: GO:0015485; F:cholesterol binding; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR001869; P:thiol_cytolysin.
 DR Pfam; PF01289; Thiol_cytolysin; 1.
 DR PRINTS; PR01400; TACTOLYSIN.
 DR PRODOM; PD007062; Thiol_cytolysin; 1.
 FT NON_TER 143
 FT NON_TER 143
 SQ SEQUENCE 143 AA; 15679 MW; 9C0BCFD3C9234FF8 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIVVERK 51
 DB 98 YIVVERK 104

RESULT 14

083U86 PRELIMINARY; PRT; 143 AA.
 AC 083U86;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DE Listeriolysin O (Fragment).
 GN Name=hlyA;
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 CC NCBI_Taxid=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CECT 935, CECT 940, CTC 1034, CECT 4032, and CECT 936;
 RX PubMed=1506755; DOI=10.1128/AEM.70.3.1366-1377.2004.
 RA Rodriguez-Lazaro D., Hernandez M., Scotti M., Beteve T., Vazquez-Boland J.A., Pla M.;
 RT "Quantitative Detection of Listeria monocytogenes and Listeria innocua by Real-time PCR: Assessment of hly, iap, and lln02483 Targets and AmpliFluor Technology.";
 RT Appl. Environ. Microbiol. 70:1366-1377(2004).
 RL Appl. Environ. Microbiol. 70:1366-1377(2004).
 DR EMBL; AY174660; AAO46018.1; -;
 DR EMBL; AY174664; AAO46022.1; -;
 DR EMBL; AY174667; AAO46025.1; -;
 DR EMBL; AY174661; AAO46019.1; -;

DR EMBL; AY174669; AA046027.1; -.
DR HSSP; P19995; IM31.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PR01400; TACTOLYSIN.
DR PRODOM; PD007062; Thiol_cytolysin; 1.
FT NON TER 143 143
SQ SEQUENCE 143 AA; 15705 MW; 71BD03A20012C5D0 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIYVERK 51
|||||
Db 98 YIYVERK 104

RESULT 15

0840A3 PRELIMINARY; PRT; 143 AA.
ID 0840A3
AC 0840A3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Listeriolysin O (Fragment).
GN Name=lytA;
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CECT 937;
RX PubMed=15006755; DOI=10.1128/AEM.70.3.1366-1377.2004;
RA Rodriguez-Lazaro D., Hernandez M., Scotti M., Esteve T.,
Vazquez-Boland J.A., Pla M.;
RT "Quantitative Detection of Listeria monocytogenes and Listeria innocua
by Real-Time PCR: Assessment of hly, iap, and lln02483 Targets and
Amplifluor Technology.";
RL Appl. Environ. Microbiol. 70:1366-1377(2004).
DR EMBL; AY174662; AA046020.1; -.
DR HSSP; P19995; IM31.
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR001869; Thiol_cytolysin.
DR Pfam; PF01289; Thiol_cytolysin; 1.
DR PRINTS; PR01400; TACTOLYSIN.
DR PRODOM; PD007062; Thiol_cytolysin; 1.
FT NON TER 143 143
SQ SEQUENCE 143 AA; 15728 MW; 432P4E14DB7F7799 CRC64;

Query Match 10.9%; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 YIYVERK 51
|||||
Db 98 YIYVERK 104

Search completed: May 4, 2005, 14:33:09
Job time : 110.847 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:03:32 ; Search time 32.3491 Seconds

(Without alignments)
191.293 Million cell updates/sec

Title: US-09-977-406a-59

Perfect score: 16
Sequence: 1 SEMQDNCERTCYET 16Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

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1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	16	5	AAO17966 Human pro
2	16	100.0	17	5	AAO17967 Human pro
3	16	100.0	18	5	AAO17968 Human pro
4	16	100.0	19	5	AAO17969 Human pro
5	16	100.0	20	5	AAO17970 Human pro
6	16	100.0	21	5	AAO17971 Human pro
7	16	100.0	22	5	AAO17972 Human pro
8	16	100.0	23	5	AAO17973 Human pro
9	16	100.0	24	5	AAO17974 Human pro
10	16	100.0	25	5	AAO17975 Human pro
11	16	100.0	26	5	AAO17976 Human pro
12	16	100.0	27	5	AAO17977 Human pro
13	16	100.0	28	5	AAO17978 Human pro
14	16	100.0	29	5	AAO17979 Human pro
15	16	100.0	30	5	AAO17980 Human pro
16	16	100.0	31	5	AAO17981 Human pro
17	16	100.0	32	5	AAO17982 Human pro
18	16	100.0	33	5	AAO17983 Human pro
19	16	100.0	34	5	AAO17984 Human pro
20	16	100.0	35	5	AAO17985 Human pro
21	16	100.0	36	5	AAO17986 Human pro
22	16	100.0	37	5	AAO17987 Human pro
23	16	100.0	38	5	AAO17988 Human pro
24	16	100.0	39	5	AAO17989 Human pro
25	16	100.0	40	5	AAO17990 Human pro

26	16	100.0	41	5	AAO17991 Human pro
27	16	100.0	42	5	AAO17992 Human pro
28	16	100.0	43	5	AAO17993 Human pro
29	16	100.0	44	5	AAO17994 Human pro
30	16	100.0	45	5	AAO17995 Human pro
31	16	100.0	94	5	AAO17911 Complete
32	16	100.0	94	5	AAO17911 Human pro
33	16	100.0	94	7	ABR56227 Native Hu
34	16	100.0	102	5	AAO17912 Human pro
35	16	100.0	102	5	ABR56228 Human pro
36	16	100.0	114	3	AAO17926 Human sec
37	16	100.0	114	4	AAU28067 Novel hum
38	16	100.0	114	6	ABR54574 Prostetic
39	16	100.0	114	7	ADB75447 Prostetic
40	16	100.0	114	7	ADB14453 Human pro
41	16	100.0	114	7	ADG26976 Human pro
42	16	100.0	114	7	ADJ68726 Human hea
43	16	100.0	114	8	ADK70534 Respirato
44	16	100.0	114	8	ADJ75600 Marker ge
45	16	100.0	114	8	ADN05811 Antipeori

ALIGNMENTS

RESULT 1
ID AAO17966 standard; peptide, 16 AA.

AC AAO17966;

DT 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #55.

EE Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

FF beta-microseminoprotein; human seminal plasma inhibin; analogue;

GG prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

HH stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

II benign prostate hyperplasia; cytostatic.

JJ Homo sapiens.

KK W0200233090-A2.

LL 25-APR-2002.

MM 15-OCT-2001; 2001WC-CA001463.

NN 16-OCT-2000; 2000CA-02321256.

OO 20-AUG-2001; 2001CA-02355334.

PP (PROC-) PROCYON BIOPHARMA INC.

QQ Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

RR WPI; 2002-471401/50.

SS New human prostate secretory protein of 94 amino acids, useful for

TT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

UU gastrointestinal, breast, endometrial, and ovarian cancers.

VV Claim 2, Page 94; 185pp; English.

WW The present invention relates to analogues of the human prostate

XX secretory protein of 94 amino acids (PSP94, also known as prostatic

YY inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

ZZ microseminoprotein (beta-MSP)). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

XX Sequence 16 AA;
SQ

Query Match 100.0%; Score 16; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEMQDNCETCTCYET 16
| | | | | | | | | | | | | | | |
Db 1 SEMQDNCETCTCYET 16

RESULT 2
AA017967
ID AA017967 standard; peptide; 17 AA.
XX
AC AA017967;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #56.

XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
OS Homo sapiens.
XX
PN WO200233090-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
DR WPI; 2002-471401/50.
XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 94; 185pp; English.

XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 16; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEMQDNCETCTCYET 16
| | | | | | | | | | | | | | | |
Db 2 SEMQDNCETCTCYET 17

RESULT 3

AA017968
ID AA017968 standard; peptide; 18 AA.
XX
AC AA017968;
XX
DT 30-AUG-2002 (first entry)
XX

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #57.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
OS Homo sapiens.
XX
PN WO200233090-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
DR WPI; 2002-471401/50.
XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 94; 185pp; English.

XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 16; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEMQDNCETCTCYET 16
| | | | | | | | | | | | | | | |
Db 3 SEMQDNCETCTCYET 18

RESULT 4
AA017969
ID AA017969 standard; peptide; 19 AA.
XX
AC AA017969;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #58.

XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX

KM benign prostate hyperplasia; cytostatic.
 XX Homo sapiens.
 XX
 XX WO200233090-A2.
 XX
 XX PD 25-APR-2002.
 XX
 XX PF 15-OCT-2001; 2001WO-CA001463.
 XX
 XX PR 16-OCT-2000; 2000CA-02321256.
 XX PR 20-AUG-2001; 2001CA-02355334.
 XX
 XX PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
 XX WPI; 2002-471401/50.
 XX
 XX PT New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX
 XX PS Claim 2; Page 95; 185pp; English.
 XX
 XX CC The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX
 XX SQ Sequence 19 AA:
 XX
 XX Query Match 100.0%; Score 16; DB 5; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 2e-11;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 SEMQTDNCETCTCYET 16
 XX |||||
 XX Db 4 SEMQTDNCETCTCYET 19
 XX
 XX RESULT 5
 XX ID AAO17970 standard; peptide; 20 AA.
 XX
 XX AC AAO17970;
 XX
 XX DT 30-AUG-2002 (first entry)
 XX
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #59.
 XX
 XX KM Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
 KM beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostate hyperplasia; cytostatic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200233090-A2.
 XX
 XX PD 25-APR-2002.
 XX
 XX PF 15-OCT-2001; 2001WO-CA001463.
 XX
 XX PR 16-OCT-2000; 2000CA-02321256.
 XX PR 20-AUG-2001; 2001CA-02355334.
 XX

PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
 XX WPI; 2002-471401/50.
 XX
 XX PT New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX
 XX PS Claim 2; Page 95; 185pp; English.
 XX
 XX CC The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX
 XX SQ Sequence 20 AA:
 XX
 XX Query Match 100.0%; Score 16; DB 5; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-11;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 SEMQTDNCETCTCYET 16
 XX |||||
 XX Db 5 SEMQTDNCETCTCYET 20
 XX
 XX RESULT 6
 XX ID AAO17971 standard; peptide; 21 AA.
 XX
 XX AC AAO17971;
 XX
 XX DT 30-AUG-2002 (first entry)
 XX
 XX DE Human prostate secretory protein of 94 amino acids PSP94 analogue #60.
 XX
 XX KM Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
 KM beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostate hyperplasia; cytostatic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200233090-A2.
 XX
 XX PD 25-APR-2002.
 XX
 XX PF 15-OCT-2001; 2001WO-CA001463.
 XX
 XX PR 16-OCT-2000; 2000CA-02321256.
 XX PR 20-AUG-2001; 2001CA-02355334.
 XX
 XX PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 XX PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
 XX WPI; 2002-471401/50.
 XX
 XX PT New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX
 XX PS Claim 2; Page 95; 185pp; English.
 XX
 XX CC The present invention relates to analogues of the human prostate

CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostatic hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 16; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQTDNCETCTCYET 16
 |||||
 DB 6 SEWQTDNCETCTCYET 21

RESULT 7
 ID AAO17972 standard; peptide; 22 AA.
 XX
 AC AAO17972;
 XX
 DT 30-AUG-2002 (first entry)
 XX

DE Human prostatic secretory protein of 94 amino acids PSP94 analogue #61.
 XX
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostatic hyperplasia; cytostatic.

XX Homo sapiens.
 XX WO200233090-A2.
 XX
 XX 25-APR-2002.
 XX
 XX 15-OCT-2001; 2001WO-CA001463.
 XX
 XX 16-OCT-2000; 2000CA-02321256.
 XX
 XX 20-AUG-2001; 2001CA-02355334.
 XX
 XX (PROC-) PROCTON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX WPI; 2002-471401/50.
 XX

DR New human prostatic secretory protein of 94 amino acids, useful for
 XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX
 PS Claim 2; Page 96; 185pp; English.

XX The present invention relates to analogues of the human prostatic
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostatic hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX

SQ Sequence 22 AA;

Query Match 100.0%; Score 16; DB 5; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.3e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQTDNCETCTCYET 16
 |||||
 DB 7 SEWQTDNCETCTCYET 22

RESULT 8
 ID AAO17973 standard; peptide; 23 AA.
 XX
 AC AAO17973;
 XX
 DT 30-AUG-2002 (first entry)
 XX

DE Human prostatic secretory protein of 94 amino acids PSP94 analogue #62.
 XX
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostatic hyperplasia; cytostatic.

XX Homo sapiens.
 XX WO200233090-A2.
 XX
 XX 25-APR-2002.
 XX
 XX 15-OCT-2001; 2001WO-CA001463.
 XX
 XX 16-OCT-2000; 2000CA-02321256.
 XX
 XX 20-AUG-2001; 2001CA-02355334.
 XX
 XX (PROC-) PROCTON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX WPI; 2002-471401/50.
 XX
 XX 25-APR-2002.
 XX
 XX 15-OCT-2001; 2001WO-CA001463.
 XX
 XX 16-OCT-2000; 2000CA-02321256.
 XX
 XX 20-AUG-2001; 2001CA-02355334.
 XX
 XX (PROC-) PROCTON BIOPHARMA INC.

XX The present invention relates to analogues of the human prostatic
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostatic hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX

SQ Sequence 23 AA;

Query Match 100.0%; Score 16; DB 5; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQTDNCETCTCYET 16
 |||||
 DB 8 SEWQTDNCETCTCYET 23

RESULT 9
 ID AAO17974 standard; peptide; 24 AA.
 XX
 AC AAO17974;
 XX
 DT 30-AUG-2002 (first entry)
 XX

Query Match 100.0%; Score 16; DB 5; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.5e-11;

DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #63.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
OS Homo sapiens.
XX
PN WO200233090-A2.
XX
PD 25-APR-2002.
XX
PP 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
DR New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 96; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
SQ Sequence 24 AA:
Query Match 100.0%; Score 16; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEMQTDNCECTCYET 16
DB 9 SEMQTDNCECTCYET 24
RESULT 10
AA017975 standard; peptide; 25 AA.
XX
AC AA017975;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #64.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
OS Homo sapiens.
XX
PN WO200233090-A2.

XX
PD 25-APR-2002.
XX
PP 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
DR New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 97; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
SQ Sequence 25 AA:
Query Match 100.0%; Score 16; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEMQTDNCECTCYET 16
DB 10 SEMQTDNCECTCYET 25
RESULT 11
AA017976 standard; peptide; 26 AA.
XX
AC AA017976;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #65.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
OS Homo sapiens.
XX
PN WO200233090-A2.
XX
PD 25-APR-2002.
XX
PP 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 97; 185pp; English.

XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention

XX Sequence 26 AA;

Query Match 100.0%; Score 16; DB 5; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.6e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEMQDNCETCTCYET 16
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 DB 11 SEMQDNCETCTCYET 26

RESULT 12
 ID AAO17977 standard; peptide; 27 AA.

XX AAO17977;

XX 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #6.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 97; 185pp; English.

XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of

CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention

XX Sequence 27 AA;

Query Match 100.0%; Score 16; DB 5; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2.7e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEMQDNCETCTCYET 16
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 DB 12 SEMQDNCETCTCYET 27

RESULT 13
 ID AAO17978 standard; peptide; 28 AA.

XX AAO17978;

XX 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #67.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 98; 185pp; English.

XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention

XX Sequence 28 AA;

Query Match 100.0%; Score 16; DB 5; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEMQDNCETCTCYET 16
 |||||
 DB 13 SEMQDNCETCTCYET 28

Thu May 5 15:11:06 2005

us-09-977-406a-59.01go.rag

Page 7

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RESULT 14
ID AAO17979 standard; peptide: 29 AA.
XX
XX AAO17979;
XX
XX 30-AUG-2002 (first entry)
XX
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #68.
DE
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
XX
XX WO200233090-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-CA001463.
XX
XX 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 98; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
XX
XX Sequence 29 AA:
SQ
Query Match 100.0%; Score 16; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEMQDNCCTCTCYET 16
Db 14 SEMQDNCCTCTCYET 29
RESULT 15
ID AAO17980 standard; peptide: 30 AA.
XX
XX AAO17980;
XX
XX 30-AUG-2002 (first entry)
XX
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #69.
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
XX

```

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XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
XX
XX WO200233090-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-CA001463.
XX
XX 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 98; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
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XX Sequence 30 AA:
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Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 15 SEMQDNCCTCTCYET 30
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Job time : 32.3491 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:13:33 ; Search time 8.20364 Seconds

(without alignments)
145.592 Million cell updates/sec

Title: US-09-977-406A-59

Sequence: 1 SEMQDNCERTCYET 16

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	94	1 US-07-899-535A-1	Sequence 1, Appl1
2	16	100.0	114	4 US-09-513-999C-7807	Sequence 7807, Ap
3	6	37.5	241	2 US-08-460-309-17	Sequence 17, Appl
4	6	37.5	241	2 US-08-125-077-17	Sequence 17, Appl
5	6	37.5	2123	4 US-09-949-016-7517	Sequence 7517, Ap
6	6	37.5	3070	4 US-09-961-403-7	Sequence 7, Appl1
7	6	37.5	3088	4 US-09-562-702A-8	Sequence 8, Appl1
8	6	37.5	3089	4 US-09-562-702A-4	Sequence 8, Appl1
9	6	37.5	3110	4 US-09-562-702A-2	Sequence 2, Appl1
10	6	37.5	3110	4 US-09-562-702A-6	Sequence 6, Appl1
11	6	37.5	3110	4 US-09-561-709B-7	Sequence 7, Appl1
12	6	37.5	3110	4 US-09-917-254-86	Sequence 86, Appl1
13	6	37.5	3110	4 US-09-949-016-5937	Sequence 5937, Ap
14	6	37.5	3111	2 US-08-460-309-4	Sequence 4, Appl1
15	6	37.5	3111	2 US-08-125-077-4	Sequence 4, Appl1
16	5	31.2	9	3 US-08-481-968A-24	Sequence 24, Appl1
17	5	31.2	9	3 US-08-154-712B-24	Sequence 24, Appl1
18	5	31.2	9	3 US-09-947-925A-24	Sequence 24, Appl1
19	5	31.2	37	4 US-09-917-340-57	Sequence 57, Appl1
20	5	31.2	37	4 US-09-829-481-11	Sequence 11, Appl1
21	5	31.2	38	4 US-09-030-619-199	Sequence 199, Ap
22	5	31.2	38	4 US-09-030-619-200	Sequence 200, Ap
23	5	31.2	58	4 US-09-621-976-5440	Sequence 5440, Ap
24	5	31.2	104	4 US-09-621-976-6750	Sequence 6750, Ap
25	5	31.2	107	4 US-09-513-999C-7986	Sequence 7986, Ap
26	5	31.2	110	4 US-09-513-999C-7055	Sequence 7055, Ap
27	5	31.2	188	4 US-09-270-767-61692	Sequence 61692, A

28	5	31.2	230	4 US-09-248-796A-21826	Sequence 21826, A
29	5	31.2	231	4 US-09-265-540E-4	Sequence 4, Appl1
30	5	31.2	231	4 US-09-717-364A-13	Sequence 13, Appl1
31	5	31.2	243	2 US-08-460-309-15	Sequence 15, Appl1
32	5	31.2	243	2 US-08-460-309-16	Sequence 16, Appl1
33	5	31.2	243	2 US-08-125-077-15	Sequence 15, Appl1
34	5	31.2	243	2 US-08-125-077-16	Sequence 16, Appl1
35	5	31.2	261	4 US-09-962-357-8	Sequence 8, Appl1
36	5	31.2	315	4 US-09-902-540-14527	Sequence 14527, A
37	5	31.2	316	4 US-09-543-681A-5873	Sequence 5873, Ap
38	5	31.2	362	4 US-09-248-796A-20514	Sequence 20514, A
39	5	31.2	392	4 US-09-424-978B-39	Sequence 39, Appl1
40	5	31.2	396	4 US-09-424-978B-36	Sequence 36, Appl1
41	5	31.2	400	4 US-09-270-767-46136	Sequence 46136, A
42	5	31.2	454	4 US-09-134-000C-5977	Sequence 5977, Ap
43	5	31.2	689	4 US-09-937-215-2	Sequence 2, Appl1
44	5	31.2	716	2 US-08-484-993B-14	Sequence 14, Appl1
45	5	31.2	716	2 US-08-484-158B-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-07-899-535A-1
Sequence 1, Application US/07899535A

Patent No. 5428011

GENERAL INFORMATION:

APPLICANT: Sheeh, Anil R.

APPLICANT: Panchal, Chandra J.

TITLE OF INVENTION: Pharmaceutical Preparations For

TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate

NUMBER OF SEQUENCES: 4 Adenocarcinoma, Stomach Cancer and Breast Cancer.

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Mr. George Loud

STREET: 2001 Jefferson Davis Highway, Suite 306

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/899,535A

FILING DATE: 16-JUN-1992

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Loud, George A.

REGISTRATION NUMBER: 25,814

REFERENCE/DOCKET NUMBER: S&B-A835

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-415-0960

TELEFAX: 703-415-0962

TELEX: 24 8614

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 94 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: protein

HYPOTHETICAL: NO

US-07-899-535A-1

Query Match 100.0%; Score 16; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEMQDNCCTCTCYET 16
Db 30 SEMQDNCCTCTCYET 45

RESULT 2
US-09-513-999C-7807
Sequence 7807, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59 US2 REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7807
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -20..-1
OTHER INFORMATION: score 9
OTHER INFORMATION: seq VLFATFVTLGNA/SC
US-09-513-999C-7807

Query Match 100.0%; Score 16; DB 4; Length 114;
Best Local Similarity 100.0%; Pred.No.3.7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEMQDNCCTCTCYET 16
Db 50 SEMQDNCCTCTCYET 65

RESULT 3
US-08-460-309-17
Sequence 17, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-17

Query Match 37.5%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred.No.5.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCCTCT 12
Db 103 NCCTCT 108

RESULT 4
US-08-125-077-17
Sequence 17, Application US/08125077
Patent No. 5872231
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
 LENGTH: 241 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-125-077-17

Query Match 37.5%; Score 6; DB 2; Length 241;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
 Db 103 NCERTCT 108

RESULT 5
 US-09-949-016-7517
 Sequence 7517, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CU001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 7517
 LENGTH: 2123
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-7517

Query Match 37.5%; Score 6; DB 4; Length 2123;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
 Db 405 NCERTCT 410

RESULT 6
 US-09-961-403-7
 Sequence 7, Application US/09961403
 Patent No. 6780594
 GENERAL INFORMATION:
 APPLICANT: HE-STUMPF, HOLGER
 APPLICANT: HAENDLER, BERNARD
 APPLICANT: KRAETZSCHMAR, JOERN
 APPLICANT: KREFT, BERTHOLD
 APPLICANT: WINTERHAGER, ELKE
 APPLICANT: REGIDOR, PEDRO
 APPLICANT: SCOTTI, SIMONE
 TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
 FILE REFERENCE: SCH-1789
 CURRENT APPLICATION NUMBER: US/09/961,403
 CURRENT FILING DATE: 2001-09-25
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 7
 LENGTH: 3070
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-961-403-7

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QY 7 NCERTCT 12
 Db 389 NCERTCT 394

RESULT 7
 US-09-562-702A-8
 Sequence 8, Application US/09562702A
 Patent No. 6632790
 GENERAL INFORMATION:
 APPLICANT: Yurchenco, Peter
 TITLE OF INVENTION: Laminin 2 and Methods for Its Use
 FILE REFERENCE: 99-274-B
 CURRENT APPLICATION NUMBER: US/09/562,702A
 CURRENT FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/155,945
 PRIOR FILING DATE: 1999-09-24
 PRIOR APPLICATION NUMBER: 60/143,289
 PRIOR FILING DATE: 1999-07-12
 PRIOR APPLICATION NUMBER: 60/139,198
 PRIOR FILING DATE: 1999-06-15
 PRIOR APPLICATION NUMBER: 60/131,720
 PRIOR FILING DATE: 1999-04-30
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 3088
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-562-702A-8

Query Match 37.5%; Score 6; DB 4; Length 3088;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
 Db 367 NCERTCT 372

RESULT 8
 US-09-562-702A-4
 Sequence 4, Application US/09562702A
 Patent No. 6632790
 GENERAL INFORMATION:
 APPLICANT: Yurchenco, Peter
 TITLE OF INVENTION: Laminin 2 and Methods for Its Use
 FILE REFERENCE: 99-274-B
 CURRENT APPLICATION NUMBER: US/09/562,702A
 CURRENT FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/155,945
 PRIOR FILING DATE: 1999-09-24
 PRIOR APPLICATION NUMBER: 60/143,289
 PRIOR FILING DATE: 1999-07-12
 PRIOR APPLICATION NUMBER: 60/139,198
 PRIOR FILING DATE: 1999-06-15
 PRIOR APPLICATION NUMBER: 60/131,720
 PRIOR FILING DATE: 1999-04-30
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 4
 LENGTH: 3089
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-562-702A-4

Query Match 37.5%; Score 6; DB 4; Length 3089;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
Db 367 NCERTCT 372

RESULT 9

US-09-562-702A-2
; Sequence 2, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-2

Query Match 37.5%; Score 6; DB 4; Length 3110;

Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
Db 389 NCERTCT 394

RESULT 10

US-09-562-702A-6
; Sequence 6, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-6

Query Match 37.5%; Score 6; DB 4; Length 3110;

Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
Db 389 NCERTCT 394

Db 389 NCERTCT 394

RESULT 11

US-09-561-709B-7
; Sequence 7, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgess, Robert
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-7

Query Match 37.5%; Score 6; DB 4; Length 3110;

Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
Db 389 NCERTCT 394

RESULT 12

US-09-917-254-86
; Sequence 86, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-86

Query Match 37.5%; Score 6; DB 4; Length 3110;

Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
Db 389 NCERTCT 394

RESULT 13

US-09-949-016-5937
; Sequence 5937, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5937
LENGTH: 3110
TYPE: PRT
ORGANISM: Human
US-09-949-016-5937

Query Match
Best Local Similarity 37.5%; Score 6; DB 4; Length 3110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NCERTCT 12
Db 389 NCERTCT 394

RESULT 14
US-08-460-309-4
Sequence 4, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE: 27-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-4

Query Match
Best Local Similarity 37.5%; Score 6; DB 2; Length 3111;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NCERTCT 12
Db 389 NCERTCT 394

RESULT 15
US-08-125-077-4
Sequence 4, Application US/08125077
Patent No. 5872231
Patent No. 5872231 5840863
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-9001
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-4

Query Match
Best Local Similarity 37.5%; Score 6; DB 2; Length 3111;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NCERTCT 12
Db 389 NCERTCT 394

Thu May 5 15:11:06 2005

us-09-977-406a-59.oligo.rai

Page 6

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Job time : 9.20364 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:33:36 ; Search time 17.8618 Seconds

(without alignments)
298.385 Million cell updates/sec

Title: US-09-977-406A-59

Sequence: 1 SEMQDNCETCTCYET 16

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published Applications MA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	16 100.0	17 10	US-09-977-406A-60	Sequence 60, Appl
3	16 100.0	18 10	US-09-977-406A-61	Sequence 61, Appl
4	16 100.0	19 10	US-09-977-406A-62	Sequence 62, Appl
5	16 100.0	20 10	US-09-977-406A-63	Sequence 63, Appl
6	16 100.0	21 10	US-09-977-406A-64	Sequence 64, Appl
7	16 100.0	22 10	US-09-977-406A-65	Sequence 65, Appl
8	16 100.0	23 10	US-09-977-406A-66	Sequence 66, Appl
9	16 100.0	24 10	US-09-977-406A-67	Sequence 67, Appl
10	16 100.0	25 10	US-09-977-406A-68	Sequence 68, Appl
11	16 100.0	26 10	US-09-977-406A-69	Sequence 69, Appl
12	16 100.0	27 10	US-09-977-406A-70	Sequence 70, Appl
13	16 100.0	28 10	US-09-977-406A-71	Sequence 71, Appl

14	16 100.0	29 10	US-09-977-406A-72	Sequence 72, Appl
15	16 100.0	30 10	US-09-977-406A-73	Sequence 73, Appl
16	16 100.0	31 10	US-09-977-406A-74	Sequence 74, Appl
17	16 100.0	32 10	US-09-977-406A-75	Sequence 75, Appl
18	16 100.0	33 10	US-09-977-406A-76	Sequence 76, Appl
19	16 100.0	34 10	US-09-977-406A-77	Sequence 77, Appl
20	16 100.0	35 10	US-09-977-406A-78	Sequence 78, Appl
21	16 100.0	36 10	US-09-977-406A-79	Sequence 79, Appl
22	16 100.0	37 10	US-09-977-406A-80	Sequence 80, Appl
23	16 100.0	38 10	US-09-977-406A-81	Sequence 81, Appl
24	16 100.0	39 10	US-09-977-406A-82	Sequence 82, Appl
25	16 100.0	40 10	US-09-977-406A-83	Sequence 83, Appl
26	16 100.0	41 10	US-09-977-406A-84	Sequence 84, Appl
27	16 100.0	42 10	US-09-977-406A-85	Sequence 85, Appl
28	16 100.0	43 10	US-09-977-406A-86	Sequence 86, Appl
29	16 100.0	44 10	US-09-977-406A-87	Sequence 87, Appl
30	16 100.0	45 10	US-09-977-406A-88	Sequence 88, Appl
31	16 100.0	94 10	US-10-291-360-1	Sequence 1, Appl
32	16 100.0	94 14	US-10-291-360-1	Sequence 1, Appl
33	16 100.0	94 17	US-10-857-358-1	Sequence 1, Appl
34	16 100.0	102 10	US-09-977-406A-2	Sequence 2, Appl
35	16 100.0	102 14	US-10-291-360-2	Sequence 2, Appl
36	16 100.0	102 17	US-10-857-358-2	Sequence 2, Appl
37	16 100.0	114 13	US-10-012-896-1003	Sequence 1003, Ap
38	16 100.0	114 14	US-10-205-823-271	Sequence 271, Ap
39	16 100.0	114 14	US-10-144-678A-1003	Sequence 1003, Ap
40	16 100.0	114 15	US-10-294-025-1003	Sequence 1003, Ap
41	16 100.0	114 15	US-10-291-172-236	Sequence 236, App
42	16 100.0	114 15	US-10-221-278-236	Sequence 236, App
43	16 100.0	114 16	US-10-408-765A-532	Sequence 532, App
44	16 100.0	132 9	US-09-925-300-1027	Sequence 1027, Ap
45	15 93.8	15 10	US-09-977-406A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-977-406A-59
; Sequence 59, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: BIOPHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHsp94 sequence (polypeptide analog)
US-09-977-406A-59

Query Match 100.0%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 9e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||
1 SEMQDNCETCTCYET 16

Db

RESULT 2
US-09-977-406A-60
; Sequence 60, Application US/09977406A

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Query Match          100.0%; Score 16; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.9e-12;
Matches      16; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY           1 SEMOTDNCETCTCYET 16
              |||||
Db            3 SEMOTDNCETCTCYET 18

RESULT 4
US-09-977-406A-62
; Sequence 62, Application US/09977406A
; Publication NO. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT : PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
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Query Match          100.0%; Score 16; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,1e-11;
Matches      16; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY           1 SEMOTDNCCTCYET 16
              |||||
Db            5 SEMOTDNCCTCYET 20

RESULT 6
US-09-977-406A-64
; Sequence 64, Application US/09977406A
; Publication NO. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT : PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 96508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
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LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-64

Query Match 100.0%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQDNCETCTCYET 16
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DB 6 SEWQDNCETCTCYET 21

RESULT 7
US-09-977-406A-65
Sequence 65, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCTON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-65

Query Match 100.0%; Score 16; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQDNCETCTCYET 16
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DB 7 SEWQDNCETCTCYET 22

RESULT 8
US-09-977-406A-66
Sequence 66, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCTON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 66
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-66

Query Match 100.0%; Score 16; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQDNCETCTCYET 16
|||||
DB 8 SEWQDNCETCTCYET 23

RESULT 9
US-09-977-406A-67
Sequence 67, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCTON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 67
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-67

Query Match 100.0%; Score 16; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQDNCETCTCYET 16
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DB 9 SEWQDNCETCTCYET 24

RESULT 10
US-09-977-406A-68
Sequence 68, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCTON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68
LENGTH: 25
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-68

Query Match 100.0%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEWQDNCETCTCYET 16
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DB 10 SEWQDNCETCTCYET 25

RESULT 11
US-09-977-406A-69
; Sequence 69, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 69
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-69

Query Match 100.0%; Score 16; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEMQDNCETCTCYET 16
Db 11 SEMQDNCETCTCYET 26

RESULT 12
US-09-977-406A-70
; Sequence 70, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 70
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-70

Query Match 100.0%; Score 16; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 1,4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEMQDNCETCTCYET 16
Db 12 SEMQDNCETCTCYET 27

RESULT 13
US-09-977-406A-71
; Sequence 71, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:

; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 71
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-71

Query Match 100.0%; Score 16; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 1,4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEMQDNCETCTCYET 16
Db 13 SEMQDNCETCTCYET 28

RESULT 14
US-09-977-406A-72
; Sequence 72, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 72
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-72

Query Match 100.0%; Score 16; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 1,5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEMQDNCETCTCYET 16
Db 14 SEMQDNCETCTCYET 29

RESULT 15
US-09-977-406A-73
; Sequence 73, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,321,256


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Query Match Similarity      100.0%; Score 16; DB 10; Length 30;
Best Local Similarity      100.0%; Pred. No. 1.5e-11;
Matches      16; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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Search completed: May 4, 2005, 15:24:08
Job time : 18.8618 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:12:38 ; Search time 5.76 Seconds
(without alignments)
267.269 Million cell updates/sec

Title: US-09-977-406a-59

Perfect score: 16

Sequence: 1 SEMQDNCFCTCYET 16

Scoring table: OLIGO

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR 79:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	114	2 A34567	beta-microseminopr
2	6	37.5	326	2 UC7094	nine-heme cytochro
3	6	37.5	601	2 B96744	unknown protein [i
4	6	37.5	895	2 T32374	hypothetical prote
5	5	31.2	38	2 JN0613	defensin 4X - scor
6	5	31.2	38	2 S27242	defensin - blue da
7	5	31.2	83	2 SS3116	methionine adenosy
8	5	31.2	91	2 SS2089	transcription fact
9	5	31.2	114	2 A54663	seminal plasma pro
10	5	31.2	130	2 S73864	hypothetical prote
11	5	31.2	130	2 G65019	hypothetical prote
12	5	31.2	167	2 C86241	protein T16B5.9 [i
13	5	31.2	210	2 AC2316	transposase alr408
14	5	31.2	246	2 A81679	conserved hypotnet
15	5	31.2	295	2 S76790	hypothetical prote
16	5	31.2	301	2 T26546	hypothetical prote
17	5	31.2	319	1 T50370	transcription fact
18	5	31.2	322	2 C70905	hypothetical prote
19	5	31.2	324	2 E83989	glutathione BH2117
20	5	31.2	334	2 D82803	glucanase hyd-3-p
21	5	31.2	347	1 B55973	transcription fact
22	5	31.2	347	2 AC0825	anaerobic sulfite
23	5	31.2	347	2 A38453	anaerobic sulfite
24	5	31.2	349	1 T50369	transcription fact
25	5	31.2	358	1 A55973	transcription fact
26	5	31.2	358	1 T51735	transcription fact
27	5	31.2	359	1 T51734	transcription fact
28	5	31.2	360	1 A55198	transcription fact
29	5	31.2	360	2 T06592	methionine adenosy

30	5	31.2	361	2 I50505	gene wnt6 protein
31	5	31.2	363	1 C55973	transcription fact
32	5	31.2	365	2 F64577	type I restriction
33	5	31.2	366	2 S66351	methionine adenosy
34	5	31.2	374	2 S41758	heat shock protein
35	5	31.2	390	2 C97058	molecular chaperon
36	5	31.2	390	2 S46540	methionine adenosy
37	5	31.2	390	2 S49491	methionine adenosy
38	5	31.2	390	2 G84785	probable s-adenosy
39	5	31.2	391	2 T43318	YNU123w protein ho
40	5	31.2	393	2 S38875	methionine adenosy
41	5	31.2	393	2 S46538	methionine adenosy
42	5	31.2	393	2 JN0131	methionine adenosy
43	5	31.2	393	2 C86155	S-adenosylmethioni
44	5	31.2	393	2 J00410	methionine adenosy
45	5	31.2	394	2 T06180	methionine adenosy

ALIGNMENTS

RESULT 1
A34567
beta-microseminoprotein precursor - human
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pro
C:Species: Homo sapiens (man)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text change 09-Jul-2004
C:Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682
R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein g
A:Reference number: A34567; MUID:90211299; PMID:232265
A:Accession: A34567
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-114 <GRE>
A:Cross-references: UNIPROT:P08118; GB:M24376; NID:G514370; PIDN:AAA59871.1; PID:G514372
R:Mitkay, M.; Nolte, S.; Fournier, S.; Benjannet, S.; Chappdelaine, P.; Paradis, G.; Dube
DNA 6, 23-29, 1987
A:Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma p
A:Reference number: A26451; MUID:87161231; PMID:3829888
A:Accession: A26451
A:Molecule type: mRNA
A:Residues: 1-114 <MEI>
A:Cross-references: GB:M15885; NID:G338414; PIDN:AAA3635.1; PID:G338415
R:Akiyama, K.; Yoshioke, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Taada, R.; Hara, M
Biochim. Biophys. Acta 829, 288-294, 1985
A:Title: The amino acid sequence of human beta-microseminoprotein.
A:Reference number: A29777; MUID:85199974; PMID:3995056
A:Accession: A29777
A:Molecule type: protein
A:Residues: 21-58, 'PT', 61-113 <AKI>
R:Seidah, N.G.; Arbatci, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.
FEBS Lett. 175, 349-355, 1984
A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction o
A:Reference number: A30984; MUID:85004133; PMID:6434350
A:Accession: A30984
A:Molecule type: protein
A:Residues: 21-112, 'G', 114 <SEI>
R:Meibler, H.; Anderson, C.; Murrie, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
Am. J. Pathol. 137, 593-604, 1990
A:Title: Beta microseminoprotein is not a prostate-specific protein.
A:Reference number: A60673; MUID:90379237; PMID:2205059
A:Accession: A60673
A:Molecule type: protein
A:Residues: 21, 'X', 23-34 <MEI>
R:Nolte, S.; Mitkay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16238
A:Molecule type: DNA

A:Residues: 1-114 <NOL>
A:Cross-references: EMBL:X57928; NID:g35760; PIRN:CAA41002.1; PID:g825707
A>Note: The authors translated the codon ACT for residue 54 as Trp
R:Lu, A.Y.; Bradner, R.C.; Vessella, R.L.
Cancer Lett. 74, 91-99, 1993
A:Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.
A:Reference number: 152662; MUID:94115955; PMID:7506990
A:Accession: 152662
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-114 <RSS>
A:Cross-references: GB:567815; NID:g460568; PIRN:AAB29732.1; PID:g460569
C:Comment: This protein is a component of seminal plasma as well as secretory fluids from
C:Genetics:
A:Gene: GDB:MSMB
A:Cross-references: GDB:128042; OMIM:157145
A:Map position: 10q11.2-10q11.2
A:Intons: 1/3; 37/1; 72/2
C:Superfamily: seminal plasma protein
C:Keywords: semen
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 100.0%; Score 6; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEMOTNCCTCTCYET 16
DB 50 SEMOTNCCTCTCYET 65

RESULT 2

JC7094
nine-heme cytochrome C - Desulfovibrio desulfuricans
C:Species: Desulfovibrio desulfuricans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: JC7094
R:Saraiya, L.M.; da Costa, P.N.; Legall, J.
Biochem. Biophys. Res. Commun. 267, 629-634, 1999
A:Title: Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774 nine-heme C
A:Reference number: JC7094; MUID:99400423; PMID:10471375
A:Accession: JC7094
A:Molecule type: DNA
A:Residues: 1-326 <SAR>
A:Cross-references: UNIPROT:Q9RNB6; GB:AF186393; NID:g5924394; PIRN:AAD56586.1; PID:g5924394
A:Experimental source: ATCC 27774
C:Genetics:
A:Gene: gHCC
C:Keywords: electron transfer; heme; heme binding

Query Match 37.5%; Score 6; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 DNCCTC 11
DB 75 DNCCTC 80

RESULT 3

B96744
unknown protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: B96744
R:Thelouis, A.; Ecker, J.R.; Palm, C.V.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ainsun, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B96744

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-601 <STO>
A:Cross-references: UNIPROT:Q9CTH2; GB:AE005173; NID:g11054407; PIRN:AA627794.1; GSPDB:GA
C:Genetics:
A:Gene: P28P5.4
A:Map position: 1

Query Match 37.5%; Score 6; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CENCCTC 13
DB 514 CENCCTC 519

RESULT 4

T32374
hypothetical protein K10F12.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
C:Accession: T32374
R:Wohlmann, P.; Beck, C.
submitted to the EMBL Data Library, September 1997
A:Description: The sequence of C. elegans cosmid K10F12.
A:Reference number: Z21157
A:Accession: T32374
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-895 <MOH>
A:Cross-references: EMBL:AF025462; PIRN:AB71005.1; GSPDB:GN00021; CESP:K10F12.3
A:Experimental source: strain Bristol N2; clone K10F12

C:Genetics:
A:Gene: CESP:K10F12.3
A:Map position: 3
A:Intons: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 624/3
C:Superfamily: Yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homology
F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X homology

Query Match 37.5%; Score 6; DB 2; Length 895;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 TDNCCT 10
DB 288 TDNCCT 293

RESULT 5

JN0613
defensin 4K - scorpion (leirus quinquestriatus)
N:Alternate names: antibacterial 4K peptide
C:Species: Leirus quinquestriatus hebraeus
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: JN0613
R:Cocciandich, S.; Goyffon, M.; Bonlemps, F.; Bulet, P.; Bouet, F.; Menez, A.; Hoffmann, J.
Biochem. Biophys. Res. Commun. 194, 17-22, 1993
A:Title: Purification and characterization of a scorpion defensin, a 4kDa antibacterial I
A:Reference number: JN0613; MUID:93326112; PMID:8333834
A:Accession: JN0613
A:Molecule type: protein
A:Residues: 1-38 <COC>

A:Cross-references: UNIPROT:P41965
A>Note: this protein is similar to scorpion toxins and insect defensins

Query Match 31.2%; Score 5; DB 2; Length 38;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 TCTCY 14
Db 32 TCTCY 36

RESULT 6

S27242
defensin - blue darter
C/Species: Aeschna cyanea (blue darter)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S27242
R/Bulet, P.; Cociancich, S.; Reuland, M.; Sauber, F.; Bischoff, R.; Hegy, G.; van Dorssse
Eur J. Biochem. 209, 977-984, 1992
A/Title: A novel insect defensin mediate the inducible antibacterial activity in larvae
A/Reference number: S27242; MUID:93049356; PMID:1425705
A/Accession: S27242
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-38 <BU>
A/Cross-references: UNIPROT:P80154

Query Match 31.2%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 TCTCY 14
Db 33 TCTCY 37

RESULT 7

S53116
methionine adenosyltransferase (EC 2.5.1.6) - chickpea (fragment)
N/Alternate names: S-adenosylmethionine synthetase
C/Species: Cicer arietinum (chickpea, garbanzo)
C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S53116
R/Cervantes, E.
submitted to the EMBL Data Library, March 1995
A/Reference number: S53116
A/Accession: S53116
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-83 <CER>
A/Cross-references: UNIPROT:Q39465; EMBL:X85252; NID:g1808591; PIDN:CAAS9508.1; PID:g732
C/Keywords: S-adenosylmethionine; transferase

Query Match 31.2%; Score 5; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 CECTCT 12
Db 43 CECTCT 47

RESULT 8

S52089
transcription factor isl-2a (clone S3) - chinook salmon
N/Alternate names: insulin enhancer-binding protein isl-2a; islet-2a protein
C/Species: Oncorhynchus tshawytscha (chinook salmon)
C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C/Accession: S52089
R/Gong, Z.; Hew, C.L.
Biochim. Biophys. Acta 1260, 349-354, 1995
A/Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus
A/Reference number: S52089; MUID:95178560; PMID:7873614
A/Accession: S52089
A/Molecule type: mRNA

A/Residues: 1-91 <GON>
A/Cross-references: EMBL:X64882
A/Experimental source: clone S3
C/Genetics:

A/Gene: isl-2a
C/Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat
C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation
F/3-56/Domain: LIM metal-binding repeat homology <LIM>

Query Match 31.2%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 ETCCTC 13
Db 40 ETCCTC 44

RESULT 9

A54663
seminal plasma protein PSP-94 precursor - rhesus macaque
N/Alternate names: prostatic secretory protein PSP94
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C/Accession: S16237; A54663
R/Nolet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A/Reference number: S16237; MUID:91274357; PMID:2054385
A/Accession: S16237
A/Molecule type: DNA
A/Residues: 1-114 <NO2>
A/Cross-references: UNIPROT:P25142; EMBL:X57932; NID:g38094; PIDN:CAA41003.1; PID:g82915;
A/Note: the authors translated the codon ACT for residue 54 as TTP
R/Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.
Genomics 9, 775-777, 1991
A/Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence bet
A/Reference number: A54663; MUID:91244325; PMID:2037304
A/Accession: A54663
A/Molecule type: mRNA
A/Residues: 1-114 <NOL>
A/Cross-references: GB:M92161; NID:g342280; PIDN:AAA36903.1; PID:g342281
C/Genetics:

A/Introns: 1/3; 37/1; 72/2
C/Superfamily: seminal plasma protein
F/1-20/Domain: signal sequence #status predicted <SIG>

Query Match 31.2%; Score 5; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 TDNCE 9
Db 54 TDNCE 58

RESULT 10

S73864
hypothetical protein H10_orf119 - Mycoplasma pneumoniae (strain ATCC 29342)
C/Species: Mycoplasma pneumoniae
A/Variety: ATCC 29342
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S73864
R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
A/Reference number: S73327; MUID:97105885; PMID:8948633
A/Accession: S73864
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-119 <HIM>
A/Cross-references: UNIPROT:P75480; EMBL:AE000052; GB:U00089; NID:g1674223; PIDN:AAB96186
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:
A:Genetic code: SGC3
C:Superfamily: holo-ACP synthase

Query Match 31.2%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 QTDNC 8
|||||
DB 21 QTDNC 25

RESULT 11

hypothetical protein b2448 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: G65019
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Berna, N.T.; Burland, V.; Riley, M.; C.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:9742617; PMID:9278503
A:Accession: G65019
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1130 <BLAT>
A:Cross-references: UNIPROT:P76548; GB:AE000332; GB:U00096; NID:g1788789; PIDN:AACT5501.
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli hypothetical protein b2448

Query Match 31.2%; Score 5; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDNCE 9
|||||
DB 43 TDNCE 47

RESULT 12

protein T16B5.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86241
R:Theologis, A.; Ecker, J.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nareau, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-167 <STO>
A:Cross-references: UNIPROT:Q9SAC5; GB:AE005172; NID:g4874271; PIDN:AAAD31336.1; GSPDB:GN
A:Genetics:
A:Gene: T16B5.9
A:Map position: 1

Query Match 31.2%; Score 5; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCYET 16
|||||

DB 91 TCYET 95

RESULT 13

transposase alr4082 [imported] - Nostoc sp. (strain PCC 7120)
AC2316
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC2316
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kurita, T.; Sasamoto, S.; Watanabe, A.; Itiguchi,
Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2316
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-210 <KUR>
A:Cross-references: UNIPROT:Q8YPV8; GB:BA000019; PIDN:BA075781.1; PID:g17133217; GSPDB:GP
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4082

Query Match 31.2%; Score 5; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWQTD 6
|||||
DB 111 EWQTD 115

RESULT 14

conserved hypothetical protein TC0662 [imported] - Chlamydia muridarum (strain Nigg)
AB1679
C:Species: Chlamydia muridarum, Chlamydia trachomatis MOPN
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: AB1679
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gall, S.R.; Heidelberg, J.F.; White, O.; Hickey, E.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MOPN and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: AB1679
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-246 <TER>
A:Cross-references: UNIPROT:Q9PK11; GB:AE002334; GB:AE002160; NID:g7190690; PIDN:AAFP3948;
A:Experimental source: strain Nigg (MOPN)
C:Genetics:
A:Gene: TC0662

Query Match 31.2%; Score 5; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCYET 16
|||||
DB 198 TCYET 202

RESULT 15

hypothetical protein - Synechocystis sp. (strain PCC 6803)
S76790
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76790
R:Kaneko, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

8.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S76790
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-295 <KAN>
 A;Cross-references: UNIPROT:P74594; EMBL:D90916; GB:AB001339; NID:G1653715; PIDN:BA41870
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Start codon: GTG
 C;Superfamily: fructosamine kinase

Query Match 31.2%; Score 5; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred.No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 WQTDN 7
 |||||
 Db 132 WQTDN 136

Search completed: May 4, 2005, 14:34:55
 Job time : 5.76 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model1

Run on: May 4, 2005, 14:04:27; Search time 27.4618 Seconds

(without alignments)
298.351 Million cell updates/sec

Title: US-09-977-406A-59

Perfect score: 16

Sequence: 1 SEWQTDNCERTCYET 16

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Word size: 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	100.0	114	1	MSMB_HUMAN
2	7	43.8	114	1	P08118 homo sapien
3	6	37.5	116	2	Q28767 papio anubi
4	6	37.5	114	1	Q90871 mus musculu
5	6	37.5	326	1	CYC9_DESDE
6	6	37.5	459	1	MURD_LACPL
7	6	37.5	601	2	Q9C7H2
8	6	37.5	1068	2	Q81A76
9	6	37.5	1075	2	Q81A75
10	6	37.5	1615	2	Q7QZU9
11	6	37.5	1870	2	Q70H34
12	6	37.5	1870	2	Q9J5A0
13	6	37.5	3110	2	Q9J5A0
14	5	31.2	37	1	DEFA_HUMAN
15	5	31.2	38	1	DEFA_ANDAU
16	5	31.2	38	1	DEFA_LEICH
17	5	31.2	51	2	DEFA_AESCY
18	5	31.2	54	2	Q7Y3N1
19	5	31.2	54	2	Q24985
20	5	31.2	58	2	Q7MGX6
21	5	31.2	69	2	Q7MGX6
22	5	31.2	69	2	Q7MGX6
23	5	31.2	70	2	Q8D1L7
24	5	31.2	74	1	DEFI_DERVA
25	5	31.2	74	1	DEFI_DERVA
26	5	31.2	75	2	Q8JX66
27	5	31.2	83	2	Q8JX67
28	5	31.2	83	2	Q8JX67
29	5	31.2	105	2	Q9J465
30	5	31.2	110	2	Q9J465
31	5	31.2	111	2	Q9J465
32	5	31.2	112	2	Q854B7

32	5	31.2	113	2	Q22079	Q22079 nicotiana t
33	5	31.2	114	1	MSMB_MACMU	P25142 macaca mla
34	5	31.2	115	2	Q7KTY0	Q7KTY0 drosophila
35	5	31.2	119	1	ACPS_MYCPN	P75480 mycoplasma
36	5	31.2	127	2	Q6IKD4	Q6IKD4 drosophila
37	5	31.2	130	1	YEFQ_ECOLI	P65448 escherichia
38	5	31.2	131	2	Q8CFP4	Q8CFP4 mus musculu
39	5	31.2	132	2	Q97442	Q97442 giardia lam
40	5	31.2	137	2	Q24987	Q24987 giardia lam
41	5	31.2	137	2	Q9W101	Q9W101 drosophila
42	5	31.2	146	2	Q86DB9	Q86DB9 heterodera
43	5	31.2	149	2	Q7PS82	Q7PS82 anopheles g
44	5	31.2	151	2	Q9UG32	Q9UG32 homo sapien
45	5	31.2	151	2	Q9F184	Q9F184 arabidopsis

ALIGNMENTS

RESULT 1
MSMB_HUMAN STANDARD; PRT; 114 AA.
ID MSMB_HUMAN
AC P08118; P11999; Q13125; Q9UC59;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).
DE Name=MSMB; Synonyms=PRSP;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=87161231; PubMed=3829888;
RA Mbikay M., Nolet S., Pournier S., Benjannet S., Chapelaine P., Paradis G., Dube J.Y., Tremblay R., Lazare C., Seidah N.G., Chretien M.;
RT "Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma protein secreted by the human prostate.";
RT DNA 6:23-29(1987).
RN [2]
RX MEDLINE=90211299; PubMed=2322265;
RA Green C.B., Liu W.Y., Kwok S.C.M.;
RT "Cloning and nucleotide sequence analysis of the human beta-microseminoprotein gene.";
RT Biochem. Biophys. Acta 1089:247-249(1991).
RN [3]
RX MEDLINE=90211299; PubMed=2322265;
RA Green C.B., Liu W.Y., Kwok S.C.M.;
RT "Cloning and nucleotide sequence analysis of the human beta-microseminoprotein gene.";
RT Biochem. Biophys. Res. Commun. 167:1184-1190(1990).
RN [4]
RX MEDLINE=90073664; PubMed=2590204;
RA Ulfvbeck M., Lindstrom C., Welber H., Abrahamsson P.-A., Lilja H., Lundwall A.;
RT "Molecular cloning of a small prostate protein, known as beta-microseminoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in non-genital tissues.";
RT Biochem. Biophys. Res. Commun. 164:1310-1315(1989).
RN [5]
RX MEDLINE=94115955; PubMed=7506990; DOI=10.1016/0304-3835(93)90049-F;
RA Liu A.Y., Bradner R.C., Vessella R.L.;
RT "Decreased expression of prostatic secretory protein PSP94 in prostate cancer.";

RL Cancer Lett. 74:91-99(1993).
 RP [6]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=Prostate; PubMed=7566962;
 RX MEDLINE=96032566; PubMed=7566962;
 RA Xuan J.W., Chin J.L., Guo Y., Chambers A.F., Finkelman M.A.,
 RA Clarke M.W.;
 RT "Alternative splicing of PSP94 (prostatic secretory protein of 94
 RT amino acids) mRNA in prostate tissue.";
 RL Oncogene 11:1041-1047(1995).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Bajjal-Gupta M., Clarke M.W.;
 RT "Prostate specific protein (PSP94) expression in a human endometrial
 RT cell line (KLE).";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buco C.K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang Y., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Peterson J.S., Carninci P., Prange C.,
 RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hele S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley A.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska T., Smalls D.E.,
 RA Schnerch A., Schein J.Z., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 2-72 FROM N.A.
 RX MEDLINE=99421644; PubMed=10491085;
 RA Maekinen M., Valtonen-Andre C., Lundvall A.;
 RT "New world, but not old world, monkeys carry several genes encoding
 RT beta-microseminoprotein.";
 RL Eur. J. Biochem. 264:407-414(1999).
 RN [10]
 RP SEQUENCE OF 21-113.
 RX MEDLINE=5519974; PubMed=3995056; DOI=10.1016/0167-4838(85)90200-6;
 RA Aitvika K., Yoshioaka Y., Schmid K., Offner G.D., Troxler R.F.,
 RA Tsuda R., Hara M.;
 RT "The amino acid sequence of human beta-microseminoprotein.";
 RL Biochim. Biophys. Acta 829:288-294(1985).
 RN [11]
 RP SEQUENCE OF 21-114.
 RX MEDLINE=85004133; PubMed=6434350; DOI=10.1016/0014-5793(84)80766-8;
 RA Seidlich N.G., Arabatti N.U., Rochemont Y., Sheeh A.R., Chretien M.;
 RT "Complete amino acid sequence of human seminal plasma beta-inhibin.
 RT Prediction of post Gln-Arg cleavage as a maturation site.";
 RL FEBS Lett. 175:349-355(1984).
 RN [12]
 RP SEQUENCE OF 21-50 AND 113-114.
 RX MEDLINE=92028964; PubMed=1930232;
 RA Liang Z.G., Kamada M., Koide S.S.;
 RT "Structural identity of immunoglobulin binding factor and prostatic
 RT secretory protein of human seminal plasma.";
 RL Biochem. Biophys. Res. Commun. 180:356-359(1991).
 RN [13]
 RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.
 RC TISSUE=Semen;
 RX MEDLINE=95401076; PubMed=7671139; DOI=10.1016/1357-2725(95)00021-G;
 RA Ohkubo I., Tada T., Ochitai Y., Ueyama H., Bimoto T., Sasaki M.;

```

RT      "Human seminal plasma beta-microseminoprotein: its purification,
RN      characterization, and immunohistochemical localization.",
RL      Int. J. Biochem. Cell Biol. 27:603-611(1995).
RP      [14].
RP      SEQUENCE OF 21-32.
RX      MEDLINE=21648993; PubMed=11788998;
RX      DOI=10.1002/1615-9861(2002012)1:1<112::AID-PROT112>3.3.CO;2-E;
RA      Ghahoui B., Stahlhofen B., Tagesson C., Lindahl M.;
RT      "Newly identified proteins in human nasal lavage fluid from non-
RT      smokers and smokers using two-dimensional gel electrophoresis and
RT      peptide mass fingerprinting.";
RL      Proteomics 2:112-120(2002).
CC      -1- SUBCELLULAR LOCATION: Secreted. Sperm surface.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=PSP4;
CC      IsoId=P08118-1; Sequence=Displayed;
CC      Name=PSP57;
CC      IsoId=P08118-2; Sequence=VSP_003275, VSP_003276;
CC      -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,
CC      breast and penis. Also expressed in pancreas, esophagus, stomach,
CC      duodenum, colon, trachea, lung, salivary glands and fallopian
CC      tube. PSP94 is expressed in lung and breast, whereas PSP57 is
CC      found in kidney and bladder.
CC      MISCELLANEOUS: Specific receptors for this protein are found on
CC      spermatozoa and in the prostate.
CC      -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC      -1- CAUTION: Was originally thought to inhibit the secretion of FSH by
CC      pituitary cells.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@lsb-sib.ch).
-----
DR      EMBL, M34376; AAAS9871.1; -.
DR      EMBL, M34373; AAAS9871.1; JOINED.
DR      EMBL, M34374; AAAS9871.1; JOINED.
DR      EMBL, M34375; AAAS9871.1; JOINED.
DR      EMBL, X57928; CAA41002.1; -.
DR      EMBL, X57929; CAA41002.1; JOINED.
DR      EMBL, X57930; CAA41002.1; JOINED.
DR      EMBL, X57931; CAA41002.1; JOINED.
DR      EMBL, S67815; AAB29732.1; -.
DR      EMBL, U22178; AAA83556.1; -.
DR      EMBL, BC005257; AAH05257.1; -.
DR      EMBL, AJ133356; CAB39325.1; -.
DR      EMBL, AF133356; CAB39325.1; -.
DR      PIR; A34567; A34567.
DR      PIR; G01730; G01730.
DR      Genew; HGNC:7372; MSMB.
DR      H-invDB: HIX0008822; -.
DR      MIM; 157145; -.
DR      GO; GO:0005615; C:extracellular space, TAS.
DR      GO; GO:0005634; C:nucleus, TAS.
DR      InterPro; IPR008735; PSP94.
DR      Pfam; PF05825; PSP94; 1.
FM      Alternative splicing; Direct protein sequencing; Polymorphism; Signal.
FT      SIGNAL 1 20
FT      CHAIN 114
FT      DISULFID 22 114 Beta-microseminoprotein.
FT      DISULFID 22 38 By similarity.
FT      DISULFID 57 93 By similarity.
FT      DISULFID 60 69 Or C-60 with C-70 (By similarity).
FT      DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT      DISULFID 84 107 By similarity.
FT      VARSPIC 37 77 KMDLDGNKHPINSQNTGNCCTCYEFISCTLVSFPY
                          -> MFHLHWMTITAKESRRRTASISWRRTRKPVLV
                          /FTid=VSP_003275.

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FT VARSPIC 78 114 Missing (in isoform PSP57).
/FTid=VSP_003276.

Query Match 100.0%; Score 16; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEMOTDNCCTCYET 16
Db 50 SEMOTDNCCTCYET 65

RESULT 2
MSMB_PAPAN STANDARD; PRT; 114 AA.

AC Q28767;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94).
GN Name=MSMB; Synonym=PSPP94;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=97316893; PubMed=9174167;
RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Mokkay M., Zhong R.,
RA Chin J.L.,
RT "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates.";
RL DNA Cell Biol. 16:627-638(1997).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface. (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U49786; AAB62726.1; -;
DR InterPro: IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
KW Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 114 Beta-microseminoprotein.
FT DISUFID 22 38 By similarity.
FT DISUFID 57 93 By similarity.
FT DISUFID 60 69 Or C-60 with C-70 (By similarity).
FT DISUFID 62 70 Or C-62 with C-69 (By similarity).
FT DISUFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98ED CRC64;

Query Match 43.8%; Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WQTDNCE 9
Db 52 WQTDNCE 58

RESULT 3
Q9DBY1 PRELIMINARY; PRT; 196 AA.
AC Q9DBY1;

DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810020E01 product:hypothetical protein, full insert
DE sequence (RIKEN CDNA 1810020E01).
GN Name=1810020E01Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,
RA Suni M., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuo M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inoue K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamori T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Wagner L., Shennan C.M., Schuler G.D.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.F., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshynski S., Carninci P., Prange C.,
 RA Bha S.S., Loughlino N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyanski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR002559; BAB25107.1; -;
 DR EMBL; BC023171; AAH23171.1; -;
 DR MGD; MGI:1913521; 1810020E01Rik.
 DR CO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR009801; DUF1370.
 DR Pfam; PF07114; DUF1370; 1.
 DR Hypothetical protein.
 KW SEQUENCE 196 AA; 21539 MW; 994DF5F251C5FEB CRC64;
 SQ
 QY 7 NCETCT 12
 Db 98 NCETCT 103
 Query Match 37.5%; Score 6; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 4
 CYC9 DESDE STANDARD; PRT; 326 AA.
 ID CYC9 DESDE
 AC Q9NR68;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Nine-heme cytochrome c precursor (9Hcc).
 OS Desulfovibrio desulfuricans.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 NCBI_TaxID=876;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99400423; PubMed=10471375; DOI=10.1006/bbr.1999.1238;
 RA Saraiva L.M., da Costa P.N., Legall U.;
 RT "Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774
 RT nine-heme cytochrome c.";
 RL Biochem. Biophys. Res. Commun. 262:629-634(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=20022508; PubMed=10555582;
 RA Matias P.M., Saraiva L.M., Soares C.M., Coelho A.V., Legall J.,
 RA Carrondo M.A.;
 RT "Nine-haem cytochrome c from Desulfovibrio desulfuricans ATCC 27774:
 RT primary sequence determination, crystallographic refinement at 1.8 Å

RT and modelling studies of its interaction with the tetrahaem cytochrome
 RT c3.";
 RT J. Biol. Inorg. Chem. 4:478-494(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99148120; PubMed=10368280; DOI=10.1016/S0969-2126(99)80019-7;
 RA Matias P.M., Coelho R., Pereira T.A.C., Coelho A.V., Thompson A.W.,
 RA Steier L., Legall U., Carrondo M.A.;
 RT "The primary and three-dimensional structures of a nine-haem
 RT cytochrome c from Desulfovibrio desulfuricans ATCC 27774 reveal a new
 RT member of the Hmc family.";
 RL Structure 7:119-130(1999).
 CC -1- FUNCTION: May form part of a transmembrane redox complex through
 CC which electrons are transferred to the cytoplasm for reduction of
 CC sulfate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- DOMAIN: Arranged into two tetraheme clusters and the extra heme 4
 CC is located asymmetrically between the two regions.
 CC -1- PTM: Binds 9 heme groups per subunit.
 CC -1- SIMILARITY: Contains 9 cytochrome c domains.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF166393; AAD56586.1; -;
 DR PIR; JC7094; JC7094
 DR PDB; 19HC; X-ray; A/B=31-322.
 DR PDB; 10FW; X-ray; A/B=31-326.
 DR PDB; 10FY; X-ray; A/B=31-326.
 DR InterPro; IPR000345; CYC heme BS.
 DR InterPro; IPR002322; Cyt CIII.
 DR InterPro; IPR011031; Multiheme cyb.
 DR Pfam; PF02085; Cytochrome CIII_1.
 DR PRINTS; PR00609; CYTOCHROME_C3.
 DR PROSITE; PS51008; MULTIHEME_CYTC; 1.
 DR 3D-structure; Electron transport; Heme; Periplasmic; Repeat; Signal.
 KW SIGNAL 1 30
 FT CHAIN 31 326 Nine-heme cytochrome c.
 FT METAL 67 67 Iron (heme 1 axial ligand).
 FT METAL 70 70 Iron (heme 3 axial ligand).
 FT BINDING 77 77 Heme 1 (covalent).
 FT BINDING 80 80 Heme 1 (covalent).
 FT METAL 81 81 Iron (heme 1 axial ligand).
 FT METAL 82 82 Iron (heme 2 axial ligand).
 FT BINDING 89 89 Heme 2 (covalent).
 FT BINDING 92 92 Heme 2 (covalent).
 FT METAL 93 93 Iron (heme 2 axial ligand).
 FT METAL 111 111 Iron (heme 5 axial ligand).
 FT BINDING 127 127 Heme 3 (covalent).
 FT BINDING 130 130 Heme 3 (covalent).
 FT METAL 131 131 Iron (heme 3 axial ligand).
 FT BINDING 141 141 Heme 4 (covalent).
 FT METAL 144 144 Heme 4 (covalent).
 FT BINDING 145 145 Iron (heme 4 axial ligand).
 FT BINDING 157 157 Heme 5 (covalent).
 FT BINDING 160 160 Heme 5 (covalent).
 FT METAL 161 161 Iron (heme 5 axial ligand).
 FT METAL 227 227 Iron (heme 6 axial ligand).
 FT METAL 230 230 Iron (heme 8 axial ligand).
 FT METAL 248 248 Iron (heme 4 axial ligand).
 FT BINDING 255 255 Heme 6 (covalent).
 FT BINDING 258 258 Heme 6 (covalent).
 FT METAL 259 259 Iron (heme 6 axial ligand).
 FT METAL 260 260 Iron (heme 7 axial ligand).
 FT BINDING 271 271 Heme 7 (covalent).
 FT BINDING 274 274 Heme 7 (covalent).

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FT METAL 275 275 Iron (heme 7 axial ligand).
FT METAL 294 294 Iron (heme 9 axial ligand).
FT BINDING 297 297 Heme 8 (covalent).
FT BINDING 300 300 Heme 8 (covalent).
FT METAL 301 301 Iron (heme 8 axial ligand).
FT BINDING 314 314 Heme 9 (covalent).
FT BINDING 317 317 Heme 9 (covalent).
FT METAL 318 318 Iron (heme 9 axial ligand).
FT STRAND 43 46
FT TURN 55 56
FT STRAND 63 66
FT HELIX 67 73
FT HELIX 77 80
FT TURN 82 83
FT TURN 89 91
FT HELIX 92 92
FT TURN 99 101
FT TURN 102 103
FT HELIX 106 111
FT HELIX 127 137
FT HELIX 139 142
FT TURN 143 143
FT HELIX 144 147
FT STRAND 154 160
FT STRAND 161 161
FT TURN 165 166
FT HELIX 169 177
FT TURN 178 178
FT HELIX 182 195
FT STRAND 204 206
FT STRAND 211 213
FT TURN 215 216
FT STRAND 220 220
FT STRAND 223 225
FT HELIX 227 236
FT TURN 237 240
FT HELIX 242 247
FT TURN 251 252
FT HELIX 253 257
FT TURN 258 258
FT HELIX 271 274
FT TURN 281 282
FT TURN 284 285
FT HELIX 289 303
FT TURN 304 305
FT TURN 311 312
FT STRAND 320 320
SQ SEQUENCE 326 AA; 35025 MW; 2ED7025ADDP250E3 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 DNCETC 11
Db 75 DNCETC 80

RESULT 5
MURD_LACPL STANDARD; PRT; 459 AA.
AC Q88V60;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (UDP-N-
  acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid
  adding enzyme).
GN Name=murd; OrderedLocName=lp_2197;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxId=1590;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RL "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
CC -1- FUNCTION: Cell wall formation. Catalyzes the addition of glutamate
CC to the nucleotide precursor UDP-N-acetyl-muramoyl-L-alanine (UMA)
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetyl-muramoyl-L-alanine +
CC glutamate = ADP + phosphate + UDP-N-acetyl-muramoyl-L-alanyl-D-
CC glutamate.
CC -1- PATHWAY: Peptidoglycan biosynthesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the murCDEF family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL935258; CAD64544.1; -
DR HSSP; P14900; 2UAG.
DR HAMAP; MF_00639; -; 1.
DR InterPro; IPR004101; Mur_ligase_C.
DR InterPro; IPR00713; Mur_ligase_N.
DR InterPro; IPR005762; MurD.
DR Pfam; PF01225; Mur_ligase; 1.
DR Pfam; PF02875; Mur_ligase_C; 1.
KW ATP-binding; Cell Division; Cell wall; Complete proteome; Ligase;
KW Peptidoglycan synthesis.
FT NP BIND 119 125 ATP (Potential).
FT SQ SEQUENCE 459 AA; 50137 MW; 083AB3E45C599DC9 CRC64;

Query Match 37.5%; Score 6; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TDNCET 10
Db 403 TDNCET 408

RESULT 6
O9C7H2 PRELIMINARY; PRT; 601 AA.
AC O9C7H2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein F28P5.4 (A1G72090/F28P5_4).
GN Name=F28P5.4;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Roming C.M., Koo H., Fujii C.Y., Uteback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

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RA Shin P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shin P., Bowser L., Carninci P.,
RA Chan M.W., Chang C.H., Dale J.M., Hayashizaki Y., Heuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL
EMBL; AC069273; AAG51137.1; -
EMBL; AF367274; AAK56263.1; -
EMBL; BT002712; AAO11628.1; -
DR
PIR; B96744; B96744.
DR
GO; GO:0003824; F: catalytic activity; IEA.
DR
GO; GO:0005506; F: iron ion binding; IEA.
DR
InterPro; IPR006638; E1p3/MiAB/NiFb.
DR
InterPro; IPR006466; Miab like B.
DR
InterPro; IPR007197; Radical_SAM.
DR
InterPro; IPR005839; UPF0004.
DR
Pfam; PF04055; Radical_SAM; 1.
DR
Pfam; PF01938; TRAM; 1.
DR
Pfam; PF00919; UPF0004; 1.
DR
SMART; SM00729; E1p3; 1.
DR
TIGRPFAM; TIGR01578; Miab-like-B; 1.
DR
TIGRPFAM; TIGR00089; UPF0004; 1.
DR
PROSITE; PS50926; TRAM; 1.
DR
PROSITE; PS01278; UPF0004; 1.
DR
Hypothetical protein.
SQ
SEQUENCE 601 AA; 65496 MW; AAC13F7EFC83DA3D CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CECTC 13
DB 514 CECTC 519

RESULT 7
Q81A76 PRELIMINARY; PRT; 1068 AA.
AC Q81A76;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform b.
GN Name=pl1-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OC NCBI_TaxID=6239;
OK NCBI_TaxID=6239;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 283:2012-2018 (1998).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

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RA Wohldmann P., Beck C.;
RT "The sequence of C. elegans cosmid K10F12.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: Contains 1 C2 domain.
DR
EMBL; AF025462; AAN72423.1; -
DR
HSSP; P10688; 1DJH.
DR
WormBase; WBGene0004045; p11-1.
DR
WormRep; K10F12.3b; CE31037.
DR
GO; GO:0004435; F: phosphoinositide phospholipase C activity; IEA.
DR
GO; GO:0007242; P: intracellular signaling cascade; IEA.
DR
GO; GO:0006629; P: lipid metabolism; IEA.
DR
InterPro; IPR000008; C2.
DR
InterPro; IPR008923; C2_CaLB.
DR
InterPro; IPR001849; PH_related.
DR
InterPro; IPR01036; PH_related.
DR
InterPro; IPR001192; PI_PLC_X.
DR
InterPro; IPR00909; PI_PLC_X.
DR
InterPro; IPR001711; PI_PLC_X.
DR
Pfam; PF00168; C2; 1.
DR
Pfam; PF00388; PI_PLC-X; 1.
DR
Pfam; PF00387; PI_PLC-X; 1.
DR
PRINTS; PR00360; C2DOMAIN.
DR
PRINTS; PR00390; PHPLIPASEC.
DR
ProDom; PD001202; PI_PLC_Y; 1.
DR
SMART; SM00239; C2; 1.
DR
SMART; SM00233; PH; 1.
DR
SMART; SM00148; PLCX; 1.
DR
SMART; SM00149; PLCY; 1.
DR
PROSITE; PS50004; C2_DOMAIN_2; 1.
DR
PROSITE; PS50007; PI_PLC_X_DOMAIN; 1.
DR
PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
SQ
SEQUENCE 1068 AA; 120042 MW; 9BF7CF9F7EC221 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDNCET 10
DB 310 TDNCET 315

RESULT 8
Q81A75 PRELIMINARY; PRT; 1075 AA.
AC Q81A75;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform a.
GN Name=pl1-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

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OC Rhabdittidae; Peloderinae; Caenorhabdittie.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 science 282:2012-2018 (1998)."
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wohldmann P., Beck C.;
 RT "The sequence of *C. elegans* cosmid K10F12."
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SMILABILITY: Contains 1 C2 domain.
 DR EMBL: AF025462; AAN72422.1; -
 DR HSSP: P10688; IDJH.
 DR WormBase: WBGene00004045; p11-1.
 DR WormPep: K10F12.3a; CE31036.
 DR GO: GO:0004435; F:Phosphoinositide phospholipase C activity; IEA.
 DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO: GO:0006629; P:lipid metabolism; IEA.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR008973; C2_CaLB.
 DR InterPro: IPR01849; PH.
 DR InterPro: IPR011036; PH_related.
 DR InterPro: IPR001192; PI_PLC.
 DR InterPro: IPR009099; PI_PLC_X.
 DR InterPro: IPR001711; PI_PLC_Y.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00388; PI_PLC_X; 1.
 DR Pfam: PF00387; PI_PLC_Y; 1.
 DR PRINTS: PR00360; C2DOMAIN.
 DR PRINTS: PR00390; PHPLIPASEC.
 DR ProDom: PD001202; PI_PLC_Y; 1.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00239; PH; 1.
 DR SMART: SM00148; PLCYC; 1.
 DR SMART: SM00149; PLCYC; 1.
 DR PROSITE: PSS0004; C2 DOMAIN 2; 1.
 DR PROSITE: PSS0007; PI_PLC_X DOMAIN; 1.
 DR PROSITE: PSS0008; PI_PLC_Y DOMAIN; 1.
 DR PROSITE: PSS0008; PI_PLC_Y DOMAIN; 1.
 SQ SEQUENCE 1075 AA; 12111 MW; 6102111ABF78AFD4 CRC64;

Query March 37.5%; Score 6; DB 2; Length 1075;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TDNCET 10
 Db 317 TDNCET 322

RESULT 9
 ID Q70Z09 PRELIMINARY; PRT; 1615 AA.
 AC Q70Z09;
 DT 01-MAR-2004 (TREMblrel. 26, Created)
 DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE GLP_609_15416_20263.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL: AACB0100040; EAA40566.1; -
 DR HSSP: P35555; IEMN.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR007742; EGF_2.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR005127; Giardia_VSP.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR002049; Laminin_EGF.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00053; Laminin_EGF; 1.
 DR Pfam: PF03302; VSP; 1.
 DR PROSITE: PS00022; EGF_1; 4.
 DR PROSITE: PS01186; EGF_2; 12.
 DR PROSITE: PS00026; EGF_3; 2.
 DR PROSITE: PS01248; LAMININ TYPE_EGF; 4.
 SQ SEQUENCE 1615 AA; 16955 MW; B88E3D60D18B4F27 CRC64;

Query March 37.5%; Score 6; DB 2; Length 1615;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DNCETC 11
 Db 1261 DNCETC 1266

RESULT 10
 ID Q70H34 PRELIMINARY; PRT; 1870 AA.
 AC Q70H34;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE VAVV Bangladesh B22R orthologue.
 OS Name=fp9.122;
 GN Fowlpox virus (isolate HP-438[Munich]).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OX NCBI_TaxID=10263;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Skinner M.A., Laidlaw S.M.;
 RT "Comparison of the genome sequence of FP9, an attenuated, tissue
 culture-adapted European fowlpox virus, with those of virulent
 American and European viruses."
 RT J. Gen. Virol. 85:305-322(2004).
 RL EMBL: AJ581527; CA852663.1; -
 DR InterPro: IPR007490; Poxvirus_B22R.
 DR Pfam: PF04395; Poxvirus_B22R; 1.
 SQ SEQUENCE 1870 AA; 211756 MW; 2423D319743D3F2F CRC64;

Query Match 37.5%; Score 6; DB 2; Length 1870;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
 Db 241 NCERTCT 246

RESULT 11
 Q9J5A0 PRELIMINARY; PRT; 1870 AA.
 AC Q9J5A0;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE ORF FPV122 varicella B22R gene family protein.
 GN Name=FPV122;
 OS Fowlpox virus (FPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Avipoxvirus.
 OC NCBI_TaxID=10261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193820; PubMed=10729156;
 RX DOI=10.1126/JVI.74.8.3815-3831.2000;
 RA Alfonso C.L., Tulman R.R., Lu Z., Zsak L., Kurish G.F., Rock D.L.;
 RT "The genome of fowlpox virus."
 RL J. Virol. 74:3815-3831(2000).
 DR EMBL; AF198100; AAF44466.1; -
 DR InterPro; IPR007490; Poxvirus_B22R.
 DR Pfam; PF04395; Poxvirus_B22R.1.
 SQ SEQUENCE 1870 AA; 211756 MW; 2423D31974D3F2F CRC64;

Query Match 37.5%; Score 6; DB 2; Length 1870;
 Best Local Similarity 100.0%; Pred. No. 80;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NCERTCT 12
 Db 241 NCERTCT 246

RESULT 12
 LMA2_HUMAN STANDARD; PRT; 3110 AA.
 ID P240Q3; Q14736; Q93022;
 AC 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain).
 DE GN Name=LMA2; Synonyms=LAMW;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94124633; PubMed=8294519; DOI=10.1083/jcb.124.3.381;
 RX Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
 RA Hyyonen H., Shows T.B., Sariola H., Hngvall E., Tryggvason K.;
 RT "Human laminin M chain (merosin): complete primary structure,
 RT RT chromosomal assignment, and expression of the M and A chain in human
 RT RT fetal tissues.";
 RL J. Cell Biol. 124:381-394(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=97066955; PubMed=8910357; DOI=10.1074/jbc.271.44.27664;
 RA Zhang X., Vuolteenaho R., Tryggvason K.,
 RT "Structure of the human laminin alpha2-chain gene (LMA2), which is

RT affected in congenital muscular dystrophy.";
 RL J. Biol. Chem. 271:27664-27669(1996).
 RN [3]
 RP SEQUENCE OF 1881-3110 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90238994; PubMed=2185464;
 RA Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Hngvall E.;
 RT "Merosin, a tissue-specific basement membrane protein, is a laminin-
 RT RT like protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
 RN [4]
 RP VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluft G.A., Amato A.A., Mendell J.R.;
 RT "Novel single base polymorphisms and rare sequence variants in the
 RT RT laminin 2-chain coding region detected by RNA/SSCP analysis.";
 RL Hum. Mutat. 13:174-174(1999).
 RN [5]
 RP ERRATUM.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluft G.A., Amato A.A., Mendell J.R.;
 RL Hum. Mutat. 13:340-340(1999).
 RN [6]
 RP VARIANT MDC1A PRO-2564.
 RX MEDLINE=21476011; PubMed=11591858;
 RX He Y., Jones K.J., Vignier N., Morgan G., Chevallay M., Barois A.,
 RA Escourret-Mathiaud B., Hori H., Mizuta T., Tome F.M.S., North K.N.,
 RA Guicheney P.;
 RT "Congenital muscular dystrophy with primary partial laminin alpha-2
 RT RT chain deficiency: molecular study.";
 RL Neurology 57:1319-1322(2001).
 RN [7]
 RP VARIANTS MDC1A TYR-527 AND ARG-862.
 RX MEDLINE=22439669; PubMed=12552556; DOI=10.1002/humu.10157;
 RX Tezak Z., Prandini P., Boscaro M., Marin A., Devaney J., Marino M.,
 RA Fanin M., Trevisan C.P., Park J., Tyson W., Finkel R., Garcia C.,
 RA Angelini C., Hoffman E.P., Pegoraro E.;
 RT "Clinical and molecular study in congenital muscular dystrophy with
 RT RT partial laminin alpha-2 (LMA2) deficiency.";
 RL Hum. Mutat. 21:103-111(2003).
 CC - FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC - SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-2 chain is a subunit of laminin-2 (merosin) and
 CC laminin-4 (S-merosin).
 CC - SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC - TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve,
 CC cardiac muscle, pancreas, lung, spleen, kidney, adrenal gland,
 CC skin, testis, meninges, choroid plexus, and some other regions of
 CC the brain, not in liver, thymus and bone.
 CC - DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC - DOMAIN: Domains VI, IV and G are globular.
 CC - DISEASE: Defects in LMA2 are the cause of merosin-deficient
 CC congenital muscular dystrophy type 1A (MDC1A) [MIM:607855]. MDC1A
 CC is characterized by difficulty walking, hypotonia, proximal
 CC weakness, hyporeflexia, and white matter hypodensity on MRI.
 CC - SIMILARITY: Contains 17 laminin EGF-like domains.
 CC - SIMILARITY: Contains 5 laminin G-like domains.
 CC - SIMILARITY: Contains 2 laminin IV domains.
 CC - SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -----
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CC -----
 DR EMBL; Z26653; CAAB1394.1; -
 DR EMBL; U66796; AAB18388.1; JOINED.
 DR EMBL; U66733; AAB18388.1; JOINED.
 DR EMBL; U66735; AAB18388.1; JOINED.
 DR EMBL; U66736; AAB18388.1; JOINED.
 DR EMBL; U66737; AAB18388.1; JOINED.
 DR EMBL; U66738; AAB18388.1; JOINED.
 DR EMBL; U66739; AAB18388.1; JOINED.
 DR EMBL; U66740; AAB18388.1; JOINED.
 DR EMBL; U66741; AAB18388.1; JOINED.
 DR EMBL; U66742; AAB18388.1; JOINED.
 DR EMBL; U66743; AAB18388.1; JOINED.
 DR EMBL; U66745; AAB18388.1; JOINED.
 DR EMBL; U66746; AAB18388.1; JOINED.
 DR EMBL; U66747; AAB18388.1; JOINED.
 DR EMBL; U66748; AAB18388.1; JOINED.
 DR EMBL; U66749; AAB18388.1; JOINED.
 DR EMBL; U66750; AAB18388.1; JOINED.
 DR EMBL; U66751; AAB18388.1; JOINED.
 DR EMBL; U66752; AAB18388.1; JOINED.
 DR EMBL; U66753; AAB18388.1; JOINED.
 DR EMBL; U66754; AAB18388.1; JOINED.
 DR EMBL; U66755; AAB18388.1; JOINED.
 DR EMBL; U66756; AAB18388.1; JOINED.
 DR EMBL; U66757; AAB18388.1; JOINED.
 DR EMBL; U66758; AAB18388.1; JOINED.
 DR EMBL; U66759; AAB18388.1; JOINED.
 DR EMBL; U66760; AAB18388.1; JOINED.
 DR EMBL; U66761; AAB18388.1; JOINED.
 DR EMBL; U66762; AAB18388.1; JOINED.
 DR EMBL; U66763; AAB18388.1; JOINED.
 DR EMBL; U66764; AAB18388.1; JOINED.
 DR EMBL; U66765; AAB18388.1; JOINED.
 DR EMBL; U66766; AAB18388.1; JOINED.
 DR EMBL; U66768; AAB18388.1; JOINED.
 DR EMBL; U66769; AAB18388.1; JOINED.
 DR EMBL; U66770; AAB18388.1; JOINED.
 DR EMBL; U66771; AAB18388.1; JOINED.
 DR EMBL; U66772; AAB18388.1; JOINED.
 DR EMBL; U66773; AAB18388.1; JOINED.
 DR EMBL; U66774; AAB18388.1; JOINED.
 DR EMBL; U66775; AAB18388.1; JOINED.
 DR EMBL; U66776; AAB18388.1; JOINED.
 DR EMBL; U66777; AAB18388.1; JOINED.
 DR EMBL; U66778; AAB18388.1; JOINED.
 DR EMBL; U66779; AAB18388.1; JOINED.
 DR EMBL; U66780; AAB18388.1; JOINED.
 DR EMBL; U66781; AAB18388.1; JOINED.
 DR EMBL; U66782; AAB18388.1; JOINED.
 DR EMBL; U66783; AAB18388.1; JOINED.
 DR EMBL; U66784; AAB18388.1; JOINED.
 DR EMBL; U66785; AAB18388.1; JOINED.
 DR EMBL; U66786; AAB18388.1; JOINED.
 DR EMBL; U66787; AAB18388.1; JOINED.
 DR EMBL; U66788; AAB18388.1; JOINED.
 DR EMBL; U66789; AAB18388.1; JOINED.
 DR EMBL; U66790; AAB18388.1; JOINED.
 DR EMBL; U66791; AAB18388.1; JOINED.
 DR EMBL; U66792; AAB18388.1; JOINED.
 DR EMBL; U66793; AAB18388.1; JOINED.
 DR EMBL; U66794; AAB18388.1; JOINED.
 DR EMBL; U66795; AAB18388.1; JOINED.
 DR EMBL; M59832; AAA63215.1; -
 DR PIR; PX0082; MATHOM.
 DR HSSP; Q60675; IDYK.
 DR Genew; HGNC:6482; LAMA2.
 DR MIM; 607855; -
 CO; GO:0005604; C:basement membrane; TAS.

DR GO; GO:0005198; F:structural molecule activity; TAS.
 DR GO; GO:0007517; P:muscle development; TAS.
 DR InterPro; IPR008985; ConA_like_1ec_g1.
 DR InterPro; IPR006209; EGF_like_g1.
 DR InterPro; IPR008979; Gal_Bind_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR000034; Laminin_B.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR009254; Laminin_I.
 DR InterPro; IPR010307; Laminin_II.
 DR InterPro; IPR008211; Laminin_N.
 DR InterPro; IPR003129; TSP_N.
 DR Pfam; PF00052; Laminin_B; 2.
 DR Pfam; PF00053; Laminin_EGF; 14.
 DR Pfam; PF00054; Laminin_G; 5.
 DR Pfam; PF06008; Laminin_I; 1.
 DR Pfam; PF06009; Laminin_II; 1.
 DR Pfam; PF00055; Laminin_N; 1.
 DR PRINTS; PR00011; EGF/LAMININ.
 DR ProDom; PD003031; Laminin_B; 2.
 DR PROSITE; PS00022; EGF_1; 11.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
 DR PROSITE; PS01248; LAMININ_TYPE_EGF; 14.
 KW Basement membrane; Cell adhesion; Coiled coil;
 KW Congenital muscular dystrophy; Direct protein sequencing;

Query Match 37.5%; Score 6; DB 1; Length 3110;
 Best Local Similarity 100.0%; Pred. No. 1;je+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NCERTCT 12
 Db 389 NCERTCT 394

RESULT 13
 ID DEF4_ANDAU STANDARD; PRT; 37 AA.
 AC P56686; P81618;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 4 kDa defensin.
 OS Androctonus australis (Sahara scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butrida; Butiidae; Androctonus.
 OX NCBI_Taxid=6858;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC STRAIN=Hector; TISSUE=Hemolymph;
 RX MEDLINE=97094646; PubMed=8939880; DOI=10.1074/jbc.271.47.29537;
 RA Ehret-Sabattier L., Loew D., Goyffon M., Fehlbauer P., Hoffmann J.A.,
 RA van Dorsselaer A., Bulet P.;
 RT "Characterization of novel cysteine-rich antimicrobial peptides from
 RT scorpion blood.";
 RL J. Biol. Chem. 271:29537-29544(1996).
 CC -1- FUNCTION: Active against Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=4206.8; METHOD=Electrospray; RANGE=1-37;
 CC NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
 CC HSSP; P80571; IFUN.
 DR InterPro; IPR001542; Defensin_anpod.
 DR Pfam; PF01097; Defensin_2; 1.
 DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.
 KW Antibiotic; Defensin; Direct protein sequencing.
 FT DISULFID 4 25 By similarity.
 FT DISULFID 11 33 By similarity.
 FT FT 15 35 By similarity.
 SO SEQUENCE 37 AA; 4212 MW; AB1363CE3FB84C1 CRC64;

Query Match 31.2%; Score 5; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TCTCY 14
 |||||
 Db 32 TCTCY 36

RESULT 14

DEF4_LEIQH STANDARD; PRT; 38 AA.
 AC P41965;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 4 kDa defensin (Antibacterial 4 kDa peptide).
 OS Leiurus quinquestriatus hebraeus (Yellow scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butrida; Butthidae; Butthidae; Leiurus.
 OX NCBI_Taxid=6884;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Hemolymph; PubMed=8333834;
 RX MEDLINE=93326112; PubMed=8333834;
 RA Cocciandich S., Gofffion M., Bontems F., Bulet P., Bouet F., Menez A.,
 Hoffmann J.A.;
 RT "Purification and characterization of a scorpion defensin, a 4kDa
 antibacterial peptide presenting structural similarities with insect
 defensins and scorpion toxins.";
 RT Biochem. Biophys. Res. Commun. 194:17-22(1993).
 CC -1- FUNCTION: Antibacterial protein against Gram-positive bacteria;
 CC may act via membrane-permeabilization of these cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
 CC PIR; JN0613; JN0613.
 DR HSSP; P80571; 1FJN.

DR InterPro; IPR001542; Defensin_2; 1.

DR Pfam; PF01097; Defensin_2; 1.

DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.

KW Antibiotic; Defensin; Direct protein sequencing.

FT DISULFID 4 25 By similarity.

FT DISULFID 11 33 By similarity.

FT DISULFID 15 35 By similarity.

SEQUENCE 38 AA; 4326 MW; DF35FB21ECB3FB64 CRC64;

Query Match 31.2%; Score 5; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TCTCY 14
 |||||
 Db 32 TCTCY 36

RESULT 15

DEF1_AESCY

ID DEF1_AESCY STANDARD; PRT; 38 AA.

AC P80154;
 DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Defensin.

OS Aeschna cyanea (Dragonfly) (Blue darner).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Paleoptera; Odonata; Anisoptera; Aeshnidae; Aeshna.

OX NCBI_Taxid=12921;
 RN [1]

RP SEQUENCE.

RC TISSUE=Hemolymph;

RX MEDLINE=93049356; PubMed=1425705;

RA Bulet P., Cocciandich S., Reuland M., Sauber F., Bischoff R., Hegy G.,
 van Dorselaer A., Hetru C., Hoffmann J.A.;

RT "A novel insect defensin mediates the inducible antibacterial activity
 in larvae of the dragonfly Aeschna cyanea (Paleoptera, Odonata).";

RT Eur. J. Biochem. 209:977-984(1992).

CC -1- FUNCTION: Mediates the inducible antibacterial activity in larvae
 of A. cyanea.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC PIR; S27242; S27242.

DR HSSP; P80571; 1FJN.

DR InterPro; IPR001542; Defensin_2; 1.

DR Pfam; PF01097; Defensin_2; 1.

DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.

KW Antibiotic; Defensin; Direct protein sequencing; Insect immunity.

FT DISULFID 4 26 By similarity.

FT DISULFID 11 34 By similarity.

FT DISULFID 15 36 By similarity.

SEQUENCE 38 AA; 4180 MW; 7C8848DF54A46A CRC64;

Query Match 31.2%; Score 5; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TCTCY 14
 |||||
 Db 33 TCTCY 37

Search completed: May 4, 2005, 14:33:10
 UOD time : 28.4618 secs

XX
SQ Sequence 45 AA;

Query Match 100.0%; Score 45; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.4e-39;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQDNCETCTCYET 45
DB 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQDNCETCTCYET 45

RESULT 2
ID AAR47117 standard; peptide; 94 AA.
XX AAR47117;
AC AAR47117;
XX 25-MAR-2003 (revised)
DT 30-JUN-1994 (first entry)
XX

Complete sequence of human prostatic inhibin peptide.

KW Prostatic inhibin peptide; cancer; adenocarcinoma; breast cancer;
KW hyperplasia; PIP; follicle stimulating hormone; FSH; tumour; inhibition;
KW prostate cancer; gastrointestinal tract.

OS Homo sapiens.

PN WO9325224-A1.

PD 23-DEC-1993.

PF 16-JUN-1993; 93MO-CA000252.

PR 16-JUN-1992; 92US-00899535.

XX (VET-) VETROGEN CORP.

PI Sheth AR, Garde S, Panchal CJ;

XX WPI, 1994-007191/01.

PT Pregm. confg. prostatic inhibin peptide or analogues - used for treating
PT benign prostatic hyperplasia, adenocarcinoma or diseases with high FSH
PT levels.

PS Disclosure; Fig 1; 48pp; English.

CC Peptides or analogues of prostatic inhibin peptide (PIP) are used in a
CC pharmaceutical preparation for treating patients with benign prostatic
CC hyperplasia or adenocarcinoma, particularly adenocarcinoma of the
CC prostate or gastrointestinal tract or breast cancer. The preparation can
CC also be used to treat patients with diseases characterised by elevated
CC levels of follicle stimulating hormone (FSH). The PIP and its analogues
CC inhibit tumour growth and decrease FSH levels without adversely affecting
CC testosterone levels. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 94 AA;

Query Match 100.0%; Score 45; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 6.2e-39;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQDNCETCTCYET 45
DB 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQDNCETCTCYET 45

RESULT 3
ID AAO17911 standard; protein; 94 AA.
XX AAO17911 standard; protein; 94 AA.

AC AAO17911;

XX 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94.

KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.

OS Homo sapiens.

PN WO200233090-A2.

PD 25-APR-2002.

PF 15-OCT-2001; 2001MO-CA001463.

PR 16-OCT-2000; 2000CA-02321256.

PR 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

PI Garde S, Panchal CJ, Bajjal-Gupta M, Frazer J, Kadhim S;

XX WPI, 2002-471401/50.

PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.

PS Disclosure; Page 73; 185pp; English.

CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is the human PSP94 protein

XX Sequence 94 AA;

Query Match 100.0%; Score 45; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 6.2e-39;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQDNCETCTCYET 45
DB 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQDNCETCTCYET 45

RESULT 4
ID ABR56227 standard; protein; 94 AA.
XX ABR56227;
AC ABR56227;
XX 20-NOV-2003 (first entry)
DT
XX

DE Native Human prostate secretory protein-94 (PSP-94).

KW Human; cytosolic; prostate secretory protein-94; PSP-94;
KW hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;
KW parathyroid hormone related peptide; PTHrP; skeletal metastasis.

OS Homo sapiens.

PN WO2003039576-A1.

XX 15-MAY-2003.
 PD 08-NOV-2002; 2002WO-CA001737.
 PF 08-NOV-2001; 2001CA-02361736.
 XX
 PR (PROC-) PROCYON BIOPHARMA INC.
 PA
 XX Rabbani SA, Shukeir N, Panchal CJ, Newman C;
 PI WPI; 2003-441476/41.
 XX
 DR Use of prostate secretory protein-94 for treating hypercalcaemia of
 PT malignancy and reducing skeletal metastasis arising from carcinomas,
 PT prostate and breast cancers.
 CC
 XX Disclosure; Page 35; 61pp; English.
 PS
 XX The present invention relates to the use of prostate secretory protein-94
 CC (PSP-94; the present sequence) for treating a patient suffering from
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,
 CC prostate and breast cancer. The PSP-94 is also useful for reducing
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need
 CC and reducing the development of skeletal metastasis. The PSP-94 is also
 CC used for the manufacture of a pharmaceutical composition for the
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis
 CC
 SQ Sequence 94 AA;
 XX
 XX
 Query Match 100.0%; Score 45; DB 7; Length 94;
 Best Local Similarity 100.0%; Pred. NO. 6.2e-39;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45
 Db 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45
 XX
 RESULT 5
 AA017912
 ID AA017912 standard; protein; 102 AA.
 XX
 AC AA017912;
 XX
 DT 30-AUG-2002. (first entry)
 DT
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #1.
 XX
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP, HSP1, beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200233090-A2.
 PD 25-APR-2002.
 PD
 PF 15-OCT-2001; 2001WO-CA001463.
 XX
 PR 16-OCT-2000; 2000CA-02321256.
 PR 20-AUG-2001; 2001CA-02355334.
 XX
 PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX WPI; 2002-471401/50.
 DR
 XX

PT New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX
 XX Claim 2; Page 73-74; 185pp; English.
 PS
 XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 CC
 SQ Sequence 102 AA;
 XX
 XX
 Query Match 100.0%; Score 45; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. NO. 6.6e-39;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 45
 Db 9 SCYFIPNEGVPDSTRKCMDLKGKHPINSEWQTDNCETCTCYET 53
 XX
 RESULT 6
 ABR56228
 ID ABR56228 standard; protein; 102 AA.
 XX
 AC ABR56228;
 XX
 DT 20-NOV-2003 (first entry)
 DT
 DE Recombinate prostate secretory protein-94 (PSP-94).
 XX
 XX Cytostatic; prostate secretory protein-94; PSP-94;
 KW hypercalcaemia of malignancy; carcinoma; prostate cancer; breast cancer;
 KW parathyroid hormone related peptide; PTHrP; skeletal metastasis.
 XX
 OS Unidentified.
 XX
 PN WO2003039576-A1.
 PD 15-MAY-2003.
 PD
 PF 08-NOV-2002; 2002WO-CA001737.
 XX
 PR 08-NOV-2001; 2001CA-02361736.
 XX
 PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 PI Rabbani SA, Shukeir N, Panchal CJ, Newman C;
 XX WPI; 2003-441476/41.
 DR
 XX Use of prostate secretory protein-94 for treating hypercalcaemia of
 PT malignancy and reducing skeletal metastasis arising from carcinomas,
 PT prostate and breast cancers.
 CC
 XX Disclosure; Page 35-36; 61pp; English.
 PS
 XX The present invention relates to the use of prostate secretory protein-94
 CC (PSP-94; the present sequence) for treating a patient suffering from
 CC hypercalcaemia of malignancy. PSP-94 is useful for treating a patient
 CC suffering from hypercalcaemia of malignancy arising from carcinomas,
 CC prostate and breast cancer. The PSP-94 is also useful for reducing
 CC parathyroid hormone related peptide (PTHrP) levels in a patient in need
 CC and reducing the development of skeletal metastasis. The PSP-94 is also
 CC used for the manufacture of a pharmaceutical composition for the
 CC treatment of hypercalcaemia of malignancy and/or skeletal metastasis
 CC

SQ Sequence 102 AA;

Query Match 100.0%; Score 45; DB 7; Length 102;
 Best Local Similarity 100.0%; Pred. No. 6.6e-39;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 45
 |||
 Db 9 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 53

RESULT 7
 AAG03726
 ID AAG03726 standard; protein; 114 AA.
 AC AAG03726;

DT 06-OCT-2000 (first entry)
 XX

DE Human secreted protein, SEQ ID NO: 7807.

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.

OS Homo sapiens.

PN EP1033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-00200610.

PR 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

PI Dumas Maïne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

XX N-PSDB; AAC03732.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 13; SEQ ID NO 7807; 71bp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors

XX Sequence, 114 AA;

Query Match 100.0%; Score 45; DB 3; Length 114;
 Best Local Similarity 100.0%; Pred. No. 7.2e-39;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 45
 |||
 Db 21 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 65

RESULT 8

AAU28067
 ID AAU28067 standard; protein; 114 AA.
 XX

AC AAU28067;

DT 18-DEC-2001 (first entry)
 XX

DE Novel human secretory protein, Seq ID No 236.

KW Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KW ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KW gut protection; lung; liver fibrosis; immune deficiency; infection;
 KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KW fertility; analgesic; pain; antigen.

OS Homo sapiens.

PN WO200166689-A2.

PD 13-SEP-2001.

PF 05-MAR-2001; 2001WO-US004942.

PR 07-MAR-2000; 2000US-00519705.

PR 19-MAY-2000; 2000US-00574454.

PR 17-JUN-2000; 2000US-00596193.

PR 14-JUL-2000; 2000US-00616847.

PR 19-SEP-2000; 2000US-00665363.

PR 20-OCT-2000; 2000US-00693267.

XX (HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;

DR Zhao Qa, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;

XX WPI; 2001-589934/66.

XX N-PSDB; AAS44967.

Example 3; SEQ ID NO 236; 107bp; English.

XX The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (II), (I) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions, ulcers,
 CC for treating osteoporosis, osteoarthritis, bone degenerative disorders,
 CC for periodontal disease. Furthermore, (I) is also useful for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic

CC reactions and conditions, such as asthma or other respiratory problems.
CC In addition, (1) affects biorhythms or circadian cycles of rhythms.
CC fertility, metabolism, catabolism, anabolism, storage or elimination of
CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
CC analogous effects or other pain reducing effects, immunoglobulin like
CC activity and can act as an antigen in a vaccine composition to raise an
CC immune response. AAU28020-AAU28395 represent novel human secreted protein
CC amino acid sequences of the invention
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 45; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
Db 21 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 9
ABR54574
ID ABR54574 standard; protein; 114 AA.
XX
AC ABR54574;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostatic secretory protein SEQ ID 1003.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KM Immune response; prostate cancer.
XX
OS Homo sapiens.
XX
PN WO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAM, Hepler WT, Hural J;
PI McNeill PD, Houghton RL, Vinals Y De Bassolac, Foy TM, Watanabe Y;
PI Deng T;
XX
DR WPI; 2003-167130/16.
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Claim 2; Page 666; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 45; DB 6; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
Db 21 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 10
ADB75447
ID ADB75447 standard; protein; 114 AA.
XX
AC ADB75447;
XX
DT 04-DEC-2003 (first entry)
XX
DE Prostate cancer marker protein.
XX
KW Prostate; cancer; cytostatic; gene therapy; marker.
XX
OS Homo sapiens.
XX
PN WO2003009814-A2.
XX
PD 06-FEB-2003.
XX
PF 25-JUL-2002; 2002WO-US023913.
XX
PR 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
PI Hoersht S, Kamatkar S, Woney AM, Glatc K, Zhao X, Anderson D;
PI WPI; 2003-248033/24.
XX
DR WPI; 2003-248033/24.
XX
PT New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
XX
PS Disclosure; SEQ ID NO 271; 99pp; English.
XX
CC The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 45; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
Db 21 SCYFIPNEGVPDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 11

ADBI4453
ID ADBI4453 standard; protein; 114 AA.
XX
AC ADBI4453;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostatic secretory protein (PSP).
XX
KW Human; prostate specific cDNA; cytostatic; immunostimulant; gene therapy;
KW cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00652729.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Kalos MD;
XX
DR WPI; 2003-756193/71.
XX
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Example 34; Page; 101p; English.
XX
XX
The invention relates to an isolated polypeptide comprising no more than
11-542 amino acids of ADBI3563 comprising a sequence ADBI4487. The
peptides comprise a fragment ADBI3563 of that contain naturally processed
T-cell epitopes for 3 class I major histocompatibility complex (MHC)
alleles. ADBI3563 is a polypeptide encoded by a human prostate specific
cDNA, one of 648 disclosed as new. Also included are nucleic acids
encoding the proteins and peptides, expression vectors, a host cell
transformed with the vector, an isolated antibody (or antigen binding
fragment) that specifically binds to the protein or peptide, detecting

CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADBI3558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a prostate specific
CC protein of the invention. Note: Except where otherwise indicated, the
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ Sequence 114 AA;

Query Match 100.0%; Score 45; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.2e-39;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPQDSTRKCMIDKGNKHPINSEWQDNCETCTCYET 45
DB 21 SCYFIPNEGVPQDSTRKCMIDKGNKHPINSEWQDNCETCTCYET 65

RESULT 12

ADG26976 ADBI4453 standard; protein; 114 AA.

ADG26976;

26-FEB-2004 (first entry)

Human prostate-specific polypeptide #243.

Human; prostate-specific polypeptide; prostate cancer; cytostatic.

Homo sapiens.

US2003157089-A1.

21-AUG-2003.

09-MAY-2002; 2002US-00144678.

XX 25-FEB-1997; 97US-00806099.
XX 01-AUG-1997; 97US-00904804.
XX 09-FEB-1998; 98US-00020956.
XX 25-FEB-1998; 98US-00030607.
XX 14-JUL-1998; 98US-00115453.
XX 23-SEP-1998; 98US-00159812.
XX 15-JAN-1999; 99US-00232149.
XX 09-APR-1999; 99US-00288946.
XX 13-JUL-1999; 99US-00352616.
XX 12-NOV-1999; 99US-00439313.
XX 18-NOV-1999; 99US-00443686.
XX 14-JAN-2000; 2000US-00483672.
XX 27-MAR-2000; 2000US-00536857.
XX 09-MAY-2000; 2000US-00568100.
XX 12-MAY-2000; 2000US-00570737.


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PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679428.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.

XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAM, Hepler WT, Hural J;
PI Mcneill PD, Houghton RL, Vinals Y De Bassolac, Foy TM, Watanabe Y;
PI Meagher MO, Deng T;
XX
XX WPI, 2003-777973/73.
XX
XX
XX PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
XX Claim 2; SEQ ID NO 1003; 99pp; English.
XX
XX The invention relates to human prostate-specific polypeptides and the
XX polynucleotides encoding them. The invention also relates to an isolated
XX antibody or its antigen-binding fragment that specifically binds a
XX polypeptide of the invention, a method of detecting cancer in a patient
XX comprising contacting a biological sample of the patient with an agent
XX that binds a prostate-specific polypeptide and comparing the amount of
XX bound polypeptide compared to a predetermined cut-off value and a fusion
XX protein comprising a prostate-specific polypeptide. The sequences of the
XX invention are used to diagnose and treat cancer, particularly prostate
XX cancer. This sequence represents a human prostate-specific polypeptide of
XX the invention. Note: The sequence data for this patent did not form part
XX of the printed specification but was obtained in electronic format
XX directly from USPTO at seqdata.uspto.gov/sequence.htm1.
XX
XX SQ Sequence 114 AA;
XX
XX Query Match 100.0%; Score 45; DB 7; Length 114;
XX Best Local Similarity 100.0%; Pred. No. 7.2e-39;
XX Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 SCYFIPNEGVPQDSTRKCMDLKGNHPIINSEMQTNDNCETCTCYET 45
XX |||||
XX Db 21 SCYFIPNEGVPQDSTRKCMDLKGNHPIINSEMQTNDNCETCTCYET 65
XX
XX
XX RESULT 13
XX ADJ68726
XX ID ADJ68726 standard; protein; 114 AA.
XX
XX ADJ68726;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human heat mitochondrial protein as a therapeutic target SeqID532.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
XX osteopathic; ophthalmological; cytosstatic.
XX
XX

```

OS	Homo sapiens.
XX	
PN	WO2003087768-A2.
XX	
PD	23-OCT-2003.
XX	
PF	04-APR-2003; 2003WO-US010870.
XX	
XX	12-APR-2002; 2002US-0372843P.
PR	17-JUN-2002; 2002US-0389987P.
PR	20-SEP-2002; 2002US-0412418P.
XX	
PA	(MITO-) MTOKOR.
PA	(BUCK-) BUCK INST AGE RES.
PI	
PI	Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI	Warnock DE;
XX	
XX	WPI; 2003-845369/78.
XX	
PT	Identifying a mitochondrial target for drug screening assays and for
PT	treating diseases associated with altered mitochondrial function,
PT	comprises detecting a modified polypeptide in a sample and correlating
PT	with the disease.
XX	
PS	Claim 1; SEQ ID NO 532; 180bp; English.
CC	
CC	This invention relates to novel mitochondrial targets that can be used
CC	for therapeutic intervention in treating a disease associated with
CC	altered mitochondrial function. Specifically, it refers to a method for
CC	identifying proteins of the human heart mitochondrial proteome that are
CC	useful for drug screening assays, as well as therapeutic targets. The
CC	present invention describes a method for identifying such proteins that
CC	can be used in the treatment of various diseases associated with altered
CC	cardiovascular function including diabetes mellitus, Huntington's disease,
CC	osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC	encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC	ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC	compositions have neuroprotective, neurotropic, antidiabetic,
CC	anticonvulsant, antiarrhythmic, osteopathic, ophthalmological and
CC	cytostatic activities. This polypeptide sequence is a human heart
CC	mitochondrial protein of the invention.
XX	
XX	Sequence 114 AA;
XX	
XX	Query Match 100.0%; Score 45; DB 7; Length 114;
XX	Best Local Similarity 100.0%; Pred. No. 7.2e-39;
XX	Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 SCVFIPNEGVPQDSTRKMDLKGKHPINSEWQTDNCETCYET 45
DB	21 SCVFIPNEGVPQDSTRKMDLKGKHPINSEWQTDNCETCYET 65
XX	
XX	RESULT 14
XX	ADK70534
XX	ID ADK70534 standard; protein; 114 AA.
XX	
XX	ADK70534;
XX	
XX	06-MAY-2004 (first entry)
XX	
XX	Respiratory disease differentially expressed protein #100.
XX	
XX	cytostatic; respiratory; antiasthmatic; gene therapy;
XX	differential gene expression; respiratory disorder; lung cancer;
XX	chronic obstructive pulmonary disease; emphysema; asthma.
XX	
XX	Homo sapiens.
XX	
XX	WO2003101283-A2.
XX	
XX	11-DEC-2003.

XX 02-JUN-2003; 2003WC-US017409.
 XX
 XX
 XX 04-JUN-2002; 2002US-0386005P.
 XX
 XX (INCY-) INCYTE CORP.
 XX
 XX Rickett PK, Krasnow R;
 XX
 XX WPI; 2004-042945/04.
 XX
 XX
 XX New combination comprising cDNAs and proteins that are differentially
 PT expressed in respiratory disorders, useful for diagnosing or treating
 PT respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
 PT diseases or asthma.
 XX
 XX
 XX Claim 14; SEQ ID NO 270; 343bp; English.
 XX
 XX The invention relates to cDNA sequences that are differentially expressed
 CC in respiratory disorders or their complements or encoded proteins. The
 CC cDNAs and proteins are useful for diagnosing, treating or monitoring
 CC treatment of a subject with a respiratory disease including lung cancer,
 CC chronic obstructive pulmonary diseases, emphysema or asthma. The protein
 CC is also useful for screening molecules or compounds to identify at least
 CC one ligand which specifically binds the protein. It is also useful for
 CC preparing and purifying a polyclonal or monoclonal antibody. This
 CC sequence corresponds to a protein of the invention.
 XX
 XX Sequence 114 AA;
 SQ
 Query Match 100.0%; Score 45; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 7.2e-39;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45
 DB 21 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 65
 RESULT 15
 ADJ75600
 ID ADJ75600 standard; protein; 114 AA.
 XX
 XX ADJ75600;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 XX
 XX Marker gene related amino acid sequence SEQ ID NO:852.
 DE
 XX bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 XX Homo sapiens.
 OS
 XX
 XX EPI394274-A2.
 PN
 XX
 XX 03-MAR-2004.
 PD
 XX
 XX 04-AUG-2003; 2003EP-00254857.
 PF
 XX
 XX 06-AUG-2002; 2002JP-00229312.
 PR
 XX 20-MAR-2003; 2003JP-00077212.
 XX
 XX (GENO-) GENOX RES INC.
 PA
 XX
 XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
 PI WPI; 2004-193155/19.
 XX
 XX
 XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a

PT healthy subject.
 XX
 XX Example 11; SEQ ID NO 852; 241bp; English.
 PS
 XX
 XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 XX Sequence 114 AA;
 SQ
 Query Match 100.0%; Score 45; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 7.2e-39;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 45
 DB 21 SCYFIPEGVPGDSTRKCMCLKGNKHPINSEWQDNCETCTCYET 65
 Search completed: May 4, 2005, 14:25:11
 Job time : 91.9818 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:13:33 ; Search time 23.0727 Seconds
(without alignments)
145.592 Million cell updates/sec

Title: US-09-977-406A-88

Sequence: 1 SCYFIPNKGVPQDSTRKCMD.....HPINSEWQTDNCCTCYET 45

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Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/1aa/5A.COMB.dep:*
- 3: /cgn2_6/ptodata/1/1aa/5B.COMB.dep:*
- 4: /cgn2_6/ptodata/1/1aa/6A.COMB.dep:*
- 5: /cgn2_6/ptodata/1/1aa/6B.COMB.dep:*
- 6: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.dep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	94	US-07-899-535A-1	Sequence 1, Appli
2	45	100.0	114	US-09-513-999C-7807	Sequence 7807, Ap
3	17	37.8	17	US-07-899-535A-3	Sequence 3, Appli
4	7	15.6	235	US-09-270-767-57304	Sequence 57304, A
5	4	15.6	514	US-09-270-767-42047	Sequence 42047, A
6	6	13.3	241	US-08-460-309-17	Sequence 17, Appli
7	6	13.3	241	US-08-125-077-17	Sequence 17, Appli
8	6	13.3	301	US-09-949-016-5524	Sequence 6524, Ap
9	6	13.3	305	US-09-949-016-5524	Sequence 9608, Ap
10	6	13.3	433	US-09-489-039A-9744	Sequence 9744, Ap
11	6	13.3	454	US-09-107-532A-4860	Sequence 4860, Ap
12	6	13.3	454	US-09-134-000C-6535	Sequence 6535, Ap
13	6	13.3	460	US-09-248-796A-19819	Sequence 19819, A
14	6	13.3	479	US-09-252-991A-19246	Sequence 19246, A
15	6	13.3	503	US-09-252-991A-27888	Sequence 27888, A
16	6	13.3	509	US-09-252-991A-23445	Sequence 23445, A
17	6	13.3	536	US-09-653-274-10	Sequence 10, Appli
18	6	13.3	536	US-10-461-791-10	Sequence 10, Appli
19	6	13.3	877	US-08-407-875-2	Sequence 2, Appli
20	6	13.3	877	US-09-126-280-2	Sequence 2, Appli
21	6	13.3	877	US-09-277-858-2	Sequence 2, Appli
22	6	13.3	929	US-09-254-594-3	Sequence 3, Appli
23	6	13.3	930	US-09-254-594-6	Sequence 6, Appli
24	6	13.3	934	US-09-949-016-10905	Sequence 10905, A
25	6	13.3	1115	US-08-568-459A-2	Sequence 2, Appli
26	6	13.3	1115	US-08-487-826B-2	Sequence 2, Appli
27	6	13.3	1115	US-09-210-288-2	Sequence 2, Appli

28	6	13.3	1115	6	5198347-6	Patent No. 5198347
29	6	13.3	1115	6	5198347-6	Patent No. 5198347
30	6	13.3	2123	4	US-09-949-016-7517	Sequence 7517, Ap
31	6	13.3	3070	4	US-09-961-403-7	Sequence 7, Appli
32	6	13.3	3088	4	US-09-562-702A-8	Sequence 8, Appli
33	6	13.3	3110	4	US-09-562-702A-2	Sequence 2, Appli
34	6	13.3	3110	4	US-09-562-702A-6	Sequence 6, Appli
35	6	13.3	3110	4	US-09-561-709B-7	Sequence 7, Appli
36	6	13.3	3110	4	US-09-917-254-86	Sequence 86, Appli
37	6	13.3	3110	4	US-09-949-016-5937	Sequence 5937, Ap
38	6	13.3	3111	2	US-08-460-309-4	Sequence 4, Appli
39	6	13.3	3111	2	US-08-125-077-4	Sequence 4, Appli
40	6	13.3	3111	2	US-09-101-272G-70	Sequence 70, Appli
41	5	11.1	5	4	US-07-791-213D-35	Sequence 35, Appli
42	5	11.1	6	1	US-08-293-150A-35	Sequence 35, Appli
43	5	11.1	6	1	US-09-101-272G-69	Sequence 69, Appli
44	5	11.1	7	1	US-07-791-213D-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-07-899-535A-1
Sequence 1, Application US/07899535A
Patent No. 5428011
GENERAL INFORMATION:
APPLICANT: Sheth, Anil R.
APPLICANT: Garde, Seema
APPLICANT: Panchal, Chandra J.
TITLE OF INVENTION: Pharmaceutical Preparations For
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mr. George Loud
STREET: 2001 Jefferson Davis Highway, Suite 306
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,535A
FILING DATE: 16-JUN-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Loud, George A.
REGISTRATION NUMBER: 25,814
REFERENCE/DOCKET NUMBER: 56B-A835
TELEPHONE: 703-415-0960
TELEFAX: 703-415-0962
TELEX: 24 8614
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-07-899-535A-1
Query Match 100.0%; Score 45; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 26-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 45
Db 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 45

RESULT 2
US-09-513-999C-7807
Sequence 7807, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59 US2 REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7807
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -20..-1
OTHER INFORMATION: score 9
OTHER INFORMATION: seq VLFAPFVTLCA/SC
US-09-513-999C-7807

Query Match 100.0%; Score 45; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 45
Db 21 SCYFIPNEGVPDSTRKMDLKGKHPINSEWOTDNCETCTCYET 65

RESULT 3
US-07-899-535A-3
Sequence 3, Application US/07899535A
Patent No. 5428011
GENERAL INFORMATION:
APPLICANT: Sheth, Anil R.
APPLICANT: Garde, Seema
APPLICANT: Panchal, Chandra J.
TITLE OF INVENTION: Pharmaceutical Preparations For
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mr. George Loud
STREET: 2001 Jefferson Davis Highway, Suite 306
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,535A
FILING DATE: 16-JUN-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Loud, George A.
REGISTRATION NUMBER: 25,814

REFERENCE/DOCKET NUMBER: S&B-A835
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-0960
TELEFAX: 703-415-0962
TELEX: 24 8614
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
MOLECULE TYPE: Peptide
TOPOLOGY: linear
HYPOTHETICAL: NO
US-07-899-535A-3

Query Match 37.8%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRK 17
Db 1 SCYFIPNEGVPDSTRK 17

RESULT 4
US-09-270-767-57304
Sequence 57304, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57304
LENGTH: 235
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-57304

Query Match 15.6%; Score 7; DB 4; Length 235;
Best Local Similarity 100.0%; Pred. No. 6.e;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LKGKHP 27
Db 33 LKGKHP 39

RESULT 5
US-09-270-767-42047
Sequence 42047, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42047
LENGTH: 514
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-42047

Query Match 15.6%; Score 7; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LKGKHP 27

Db 312 LKGNKHP 318

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RESULT 6
US-08-460-309-17
; Sequence 17, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leiyo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELEPHONE: (619) 535-9001
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-460-309-17

Query Match 13.3%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 36 NCETCT 41
Db 103 NCETCT 108

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RESULT 7
US-08-125-077-17
; Sequence 17, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leiyo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
```

```
|||||
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; TELEPHONE: (619) 535-9001
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-125-077-17

Query Match 13.3%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 36 NCETCT 41
Db 103 NCETCT 108

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RESULT 8
US-09-949-016-6524
; Sequence 6524, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6524
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Human
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US-09-949-016-6524

Query Match

Best Local Similarity 13.3%; Score 6; DB 4; Length 301;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGDSTR 16

DB 81 PGDSTR 86

RESULT 9

US-09-949-016-9608
Sequence 9608, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9608
LENGTH: 305
TYPE: PRT
ORGANISM: Human
US-09-949-016-9608

Query Match

Best Local Similarity 13.3%; Score 6; DB 4; Length 305;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PGDSTR 16

DB 85 PGDSTR 90

RESULT 10

US-09-489-039A-9744
Sequence 9744, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9744
LENGTH: 433
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9744

Query Match

Best Local Similarity 13.3%; Score 6; DB 4; Length 433;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGNKHP 27

DB 264 KGNKHP 269

RESULT 11

US-09-107-532A-4860
Sequence 4860, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4860:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...454
SEQUENCE DESCRIPTION: SEQ ID NO: 4860:
US-09-107-532A-4860

Query Match 13.3%; Score 6; DB 4; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNK 25

DB 222 DLKGNK 227

RESULT 12

US-09-134-000C-6535

Sequence 6535, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

PRIOR FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 6535
 LENGTH: 454
 TYPE: PRT
 ORGANISM: Enterococcus faecalis
 US-09-134-000C-6535

Query Match 13.3%; Score 6; DB 4; Length 454;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNK 25
 DB 222 DLKGNK 227

RESULT 13
 US-09-248-796A-19819
 Sequence 19819, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Kelch Weinstein et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 19819
 LENGTH: 460
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-19819

Query Match 13.3%; Score 6; DB 4; Length 460;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGVPGD 13
 DB 301 EGVPGD 306

RESULT 14
 US-09-252-991A-19246
 Sequence 19246, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 19246
 LENGTH: 479
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19246

Query Match 13.3%; Score 6; DB 4; Length 479;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 PGDSTR 16
 DB 19 PGDSTR 24

RESULT 15
 US-09-252-991A-27888
 Sequence 27888, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 27888
 LENGTH: 503
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-27888

Query Match 13.3%; Score 6; DB 4; Length 503;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NEGVPG 12
 DB 123 NEGVPG 128

Search completed: May 4, 2005, 14:37:23
 Job time : 23.0727 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:33:36 ; Search time 50.2364 Seconds
(without alignments)
298.385 Million cell updates/sec

Title: US-09-977-406a-88

Perfect score: 45

Sequence: 1 SCFFINEGVPGDSTRKCMD.....HPINSEWQTDNCFCTCYET 45

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	45	US-09-977-406a-88	Sequence 88, Appl
2	45	100.0	94	US-09-977-406a-1	Sequence 1, Appl
3	45	100.0	94	US-10-291-360-1	Sequence 1, Appl
4	45	100.0	94	US-10-857-358-1	Sequence 1, Appl
5	45	100.0	102	US-09-977-406a-2	Sequence 2, Appl
6	45	100.0	102	US-10-291-360-2	Sequence 2, Appl
7	45	100.0	102	US-10-857-358-2	Sequence 2, Appl
8	45	100.0	114	US-10-012-896-1003	Sequence 1003, Ap
9	45	100.0	114	US-10-205-823-271	Sequence 271, App
10	45	100.0	114	US-10-144-678A-1003	Sequence 1003, Ap
11	45	100.0	114	US-10-294-025-1003	Sequence 1003, Ap
12	45	100.0	114	US-10-291-172-236	Sequence 236, App
13	45	100.0	114	US-10-221-278-236	Sequence 236, App

14	45	100.0	114	US-10-408-765A-532	Sequence 532, App
15	45	100.0	132	US-09-925-300-1027	Sequence 1027, Ap
16	44	97.8	44	US-09-977-406a-87	Sequence 87, Appl
17	43	95.6	43	US-09-977-406a-86	Sequence 86, Appl
18	42	93.3	42	US-09-977-406a-85	Sequence 85, Appl
19	41	91.1	41	US-09-977-406a-84	Sequence 84, Appl
20	40	88.9	40	US-09-977-406a-83	Sequence 83, Appl
21	39	86.7	39	US-09-977-406a-82	Sequence 82, Appl
22	38	84.4	38	US-09-977-406a-81	Sequence 81, Appl
23	37	82.2	37	US-09-977-406a-80	Sequence 80, Appl
24	36	80.0	36	US-09-977-406a-79	Sequence 79, Appl
25	35	77.8	35	US-09-977-406a-78	Sequence 78, Appl
26	34	75.6	34	US-09-977-406a-77	Sequence 77, Appl
27	33	73.3	33	US-09-977-406a-76	Sequence 76, Appl
28	32	71.1	32	US-09-977-406a-75	Sequence 75, Appl
29	31	68.9	31	US-09-977-406a-74	Sequence 74, Appl
30	30	66.7	30	US-09-977-406a-73	Sequence 73, Appl
31	29	64.4	29	US-09-977-406a-72	Sequence 72, Appl
32	29	64.4	119	US-10-291-172-612	Sequence 612, App
33	29	64.4	119	US-10-221-278-612	Sequence 612, App
34	28	62.2	28	US-09-977-406a-71	Sequence 71, Appl
35	27	60.0	27	US-09-977-406a-70	Sequence 70, Appl
36	26	57.8	26	US-09-977-406a-69	Sequence 69, Appl
37	25	55.6	25	US-09-977-406a-68	Sequence 68, Appl
38	24	53.3	24	US-09-977-406a-67	Sequence 67, Appl
39	23	51.1	23	US-09-977-406a-66	Sequence 66, Appl
40	22	48.9	22	US-09-977-406a-65	Sequence 65, Appl
41	21	46.7	21	US-09-977-406a-64	Sequence 64, Appl
42	20	44.4	20	US-09-977-406a-63	Sequence 63, Appl
43	19	42.2	19	US-09-977-406a-62	Sequence 62, Appl
44	18	40.0	18	US-09-977-406a-61	Sequence 61, Appl
45	17	37.8	17	US-09-977-406a-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1

US-09-977-406a-88

Sequence 88, Application US/09977406A

Publication No. US20030170220A1

GENERAL INFORMATION:

APPLICANT: PROCYON PHARMACEUTICAL INC.

TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS

FILE REFERENCE: 06508-030-US-03

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256

PRIOR FILING DATE: 2000-10-16

PRIOR APPLICATION NUMBER: CA 2,355,334

PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PatentIn version 3.1

SEQ ID NO 88

LENGTH: 45

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Polypeptide derived from rHUPSP94 sequence (polypeptide analog)

US-09-977-406a-88

Query Match 100.0%; Score 45; DB 10; Length 45;

Best Local Similarity 100.0%; Pred. No. 5.1e-41;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCFFINEGVPGDSTRKCMDLKGKHPINSEWQTDNCFCTCYET 45

Db 1 SCFFINEGVPGDSTRKCMDLKGKHPINSEWQTDNCFCTCYET 45

RESULT 2

US-09-977-406a-1

Sequence 1, Application US/09977406A

Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and
AUTHORS: Lundwall, A.
TITLE: Molecular cloning of a small prostate protein, known as beta-
TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in
TITLE: non-genital tissues.
JOURNAL: Biochem. Biophys. Res Commun.
VOLUME: 164
ISSUE: 3
PAGES: 1310-1315
DATE: 1989
DATABASE ACCESSION NUMBER: GI 131436
DATABASE ENTRY DATE: 1988-08-01
US-09-977-406A-1

Query Match 100.0%; Score 45; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 9,7e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCETCTCYET 45
DB 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCETCTCYET 45

RESULT 3
US-10-291-360-1
Sequence 1, Application US/10291360
Publication No. US20030119744A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-051-US-02
CURRENT APPLICATION NUMBER: US/10/291,360
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and
AUTHORS: Lundwall, A.
TITLE: Molecular cloning of a small prostate protein, known as beta-
TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in
TITLE: non-genital tissues.
JOURNAL: Biochem. Biophys. Res Commun.
VOLUME: 164
ISSUE: 3
PAGES: 1310-1315
DATE: 1989
DATABASE ACCESSION NUMBER: GI 131436
DATABASE ENTRY DATE: 1988-08-01
US-10-291-360-1

Query Match 100.0%; Score 45; DB 14; Length 94;
Best Local Similarity 100.0%; Pred. No. 9,7e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCETCTCYET 45
DB 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCETCTCYET 45

RESULT 4
US-10-857-358-1
Sequence 1, Application US/10857358
Publication No. US20050026833A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-153
CURRENT APPLICATION NUMBER: US/10/857,358
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 10/291,360
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Ulvback, M., Lindstrom, C., Welber, H., Abrahamson, P.A., Lilja, H., and
AUTHORS: Lundwall, A.
TITLE: Molecular cloning of a small prostate protein, known as beta-
TITLE: microsemoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in
TITLE: non-genital tissues.
JOURNAL: Biochem. Biophys. Res Commun.
VOLUME: 164
ISSUE: 3
PAGES: 1310-1315
DATE: 1989
DATABASE ACCESSION NUMBER: GI 131436
DATABASE ENTRY DATE: 1988-08-01
US-10-857-358-1

Query Match 100.0%; Score 45; DB 17; Length 94;
Best Local Similarity 100.0%; Pred. No. 9,7e-41;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCETCTCYET 45
DB 1 SCYFIPNEGVPDSTRKMDLKGKHPINSEWQTDNCETCTCYET 45

RESULT 5
US-09-977-406A-2
Sequence 2, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 102
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: recombinant human PSP94 (rhPSP94) produced from yeast
US-09-977-406A-2

Query Match 100.0%; Score 45; DB 10; Length 102;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
Db 9 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 53

RESULT 6
US-10-291-360-2
Sequence 2, Application US/10291360
Publication No. US20030119744A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-051-US-02
CURRENT APPLICATION NUMBER: US/10/291,360
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 102
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: recombinant human PSP94 (rhPSP94) produced from yeast
US-10-291-360-2

Query Match 100.0%; Score 45; DB 14; Length 102;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
Db 9 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 53

RESULT 7
US-10-857-358-2
Sequence 2, Application US/10857358
Publication No. US2005026833A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PSP-94: Use for Treatment of Hypercalcemia and Bone metastasis
FILE REFERENCE: 06508-153
CURRENT APPLICATION NUMBER: US/10/857,358
CURRENT FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: CA 2,361,736
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 10/291,360
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 102
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: recombinant human PSP94 (rhPSP94) produced from yeast
US-10-857-358-2

Query Match 100.0%; Score 45; DB 17; Length 102;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
Db 9 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 53

RESULT 8
US-10-012-896-1003
Sequence 1003, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuguo
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1003
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-896-1003

Query Match 100.0%; Score 45; DB 13; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
Db 21 SCFFIPNEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 9
US-10-205-823-271
Sequence 271, Application US/10205823
Publication No. US20030108963A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 271
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-271

Query Match 100.0%; Score 45; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 45
DB 21 SCYFIPEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 65

RESULT 10
US-10-144-678A-1003
Sequence 1003, Application US/10144678A
Publication No. US20030157089A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Uiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals Y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Matanabe, Yoshinobu
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1003
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-144-678A-1003

Query Match 100.0%; Score 45; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 45
DB 21 SCYFIPEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 65

RESULT 11
US-10-294-025-1003
Sequence 1003, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Stolk, John A.
APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1003
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-294-025-1003

Query Match 100.0%; Score 45; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 45
DB 21 SCYFIPEGVPDSTRKCMDLKGKHPINSEWQDNCETCTCYET 65

RESULT 12
US-10-291-172-236
Sequence 236, Application US/10291172
Publication No. US20030228584A1
GENERAL INFORMATION:
APPLICANT: Hysed, Inc
TITLE OF INVENTION: No. US20030228584A1 Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/291,172
CURRENT FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,847
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 236
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
US-10-291-172-236

Query Match 100.0%; Score 45; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
|||||
Db 21 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 13
US-10-221-278-236
; Sequence 236, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 236
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-221-278-236

Query Match 100.0%; Score 45; DB 15; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
|||||
Db 21 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65

RESULT 14
US-10-408-765A-532
; Sequence 532, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 532
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-532

Query Match 100.0%; Score 45; DB 16; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45

Db 21 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 65
|||||

RESULT 15
US-09-925-300-1027
; Sequence 1027, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruden,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1690
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1027
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1027

Query Match 100.0%; Score 45; DB 9; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 45
|||||
Db 39 SCYFIPEGVPGDSTRCKMDLKGKHPINSEWQTDNCETCTCYET 83

Search completed: May 4, 2005, 15:24:08
Job time : 50.2364 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:12:38 ; Search time 16.2 Seconds

(without alignments)
267.269 Million cell updates/sec

Title: US-09-977-406A-88

Sequence: 1 SCFFIPNPGVPGSDSTRKCMD.....HPINSEWQTNCECTCYET 45

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: PIR 79: *
2: p1r1: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	114	2 A34567	beta-microseminopr
2	16	35.6	77	2 G01730	PSF57 - human
3	11	24.4	114	2 A54663	seminal plasma pro
4	7	15.6	93	2 AF0776	conserved hypotet
5	7	15.6	502	2 D70806	probable fadD17 pr
6	6	13.3	91	2 S41663	beta-microseminopr
7	6	13.3	105	2 PC4046	hypothetical 105 p
8	6	13.3	160	2 H86662	thiol peroxidase (
9	6	13.3	215	2 T41423	hypothetical prote
10	6	13.3	226	2 T49719	hypothetical prote
11	6	13.3	239	2 D71187	probable ribosomal
12	6	13.3	324	2 AF1279	hypothetical prote
13	6	13.3	326	2 UC7034	nine-heme cytochro
14	6	13.3	405	2 D96614	hypothetical prote
15	6	13.3	458	2 S41593	translation elonga
16	6	13.3	460	2 A31514	translation elonga
17	6	13.3	460	2 S43861	translation elonga
18	6	13.3	468	2 T50982	origin recognition
19	6	13.3	495	2 C83358	hypothetical prote
20	6	13.3	497	2 B71677	histidine kinase s
21	6	13.3	497	2 G97738	histidine kinase s
22	6	13.3	525	2 T34556	hypothetical prote
23	6	13.3	570	2 T38489	helicase - fisson
24	6	13.3	601	2 B96744	unknown protein [i
25	6	13.3	803	2 E82392	phosphoenolpyruvat
26	6	13.3	871	2 A46742	metabotropic gluta
27	6	13.3	881	2 T33810	metabotropic prote
28	6	13.3	895	2 T32374	hypothetical prote
29	6	13.3	900	2 C96842	hypothetical prote

30	6	13.3	960	2 S54461	hypothetical prote
31	6	13.3	966	2 G69189	hypothetical prote
32	6	13.3	1070	2 T30848	Duffy receptor - P
33	6	13.3	1140	2 T24213	hypothetical prote
34	6	13.3	1295	2 A32901	gip1 protein precu
35	6	13.3	1460	2 T00095	hypothetical prote
36	6	13.3	1496	2 T19833	hypothetical prote
37	6	13.3	1696	2 T23617	hypothetical prote
38	6	13.3	3328	2 T30835	breast cancer tumo
39	6	13.3	3329	2 T42205	breast cancer susc
40	6	13.3	3329	2 T30904	breast cancer tumo
41	5	11.1	18	2 T13132	protein gp45.1 - p
42	5	11.1	20	2 S00492	hemocyanin chain I
43	5	11.1	35	2 G60529	hemocyanin M3' - c
44	5	11.1	36	2 A38729	pyruvate decarboxy
45	5	11.1	38	2 JN0613	defensin 4K - scor

ALIGNMENTS

RESULT 1
A34567
beta-microseminoprotein precursor - human
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pro
C:Species: Homo sapiens (man)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682
R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein g
A:Reference number: A34567; MUID:90211299; PMID:2322265
A:Accession: A34567
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-114 <GRB>
A:Cross-references: UNIPROT:P08118; GB:M34376; NID:G514370; PIDN:AAA59871.1; PID:G514372
R:Mitkay, M.; Nolec, S.; Fournier, S.; Benjannet, S.; Chappdelaine, P.; Paradis, G.; Dube
DNA 6, 23-29, 1987
A:Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma p
A:Reference number: A26451; MUID:87161231; PMID:3829888
A:Accession: A26451
A:Molecule type: mRNA
A:Residues: 1-114 <MBI>
A:Cross-references: GB:M15885; NID:G338414; PIDN:AAA3635.1; PID:G338415
R:Akiyama, K.; Yoshiooka, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara, M
Biochim. Biophys. Acta 829, 288-294, 1985
A:Title: The amino acid sequence of human beta-microseminoprotein.
A:Reference number: A29777; MUID:85199974; PMID:3995056
A:Accession: A29777
A:Molecule type: protein
A:Residues: 21-58, 'P', 61-113 <AKI>
R:Seidah, N.G.; Arbatli, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.
FEBS Lett. 175, 349-355, 1984
A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction o
A:Reference number: A30984; MUID:85004133; PMID:6434350
A:Accession: A30984
A:Molecule type: protein
A:Residues: 21-112, 'G', 114 <SEI>
R:Weiber, H.; Anderson, C.; Murine, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
Am. J. Pathol. 117, 593-604, 1990
A:Title: Beta microseminoprotein is not a prostate-specific protein.
A:Reference number: A60673; MUID:90379237; PMID:2205099
A:Accession: A60673
A:Molecule type: protein
A:Residues: 21, 'X', 23-34 <WEI>
A:Experimental source: gastric juice
R:Nolec, S.; Mitkay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16238
A:Molecule type: DNA

A:Residues: 1-114 <NOL>
A:Cross-references: EMBL:X57928; NID:g35760; PIDN:CAA1002.1; PID:g825707
A:Note: the authors translated the codon ACT for residue 54 as TTP
R:Li, A.Y.; Bradner, R.C.; Vessella, R.L.
Cancer Lett. 74, 91-99, 1993
A:Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.
A:Reference number: 152682; MUID:94115955; PMID:7506990
A:Accession: 152682
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-114 <RNS>
A:Cross-references: GB:S67915; NID:g460568; PIDN:AAB29732.1; PID:g460569
C:Comment: This protein is a component of seminal plasma as well as secretory fluids from
C:Genetics:
A:Gene: GDB:MSMB
A:Cross-references: GDB:128042; OMIM:157145
A:Map position: 10q11.2-10q11.2
A:Intons: 1/3; 37/1; 72/2
C:Superfamily: seminal plasma protein
C:Keywords: semen
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 100.0%; Score 45; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFENEGVPGDSTR 16
|||||
DB 21 SCVFENEGVPGDSTR 36

RESULT 2
G01730
PSP57 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G01730
R:Xuan, J.W.; Chin, J.D.; Guo, Y.; Chamber, A.F.; Finkelstein, M.A.; Clarke, M.W.
submitted to the EMBL Data Library, March 1995
A:Reference number: G08240
A:Accession: G01730
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-77 <XUA>
A:Cross-references: UNIPROT:P08118; EMBL:U22178; NID:g885984; PIDN:AAA83556.1; PID:g8859
C:Superfamily: seminal plasma protein

Query Match 35.6%; Score 16; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCVFENEGVPGDSTR 16
|||||
DB 21 SCVFENEGVPGDSTR 36

RESULT 3
A54663
seminal plasma protein PSP-94 precursor - rhesus macaque
N:Alternate names: prostatic secretory protein PSP94
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
R:Nolet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16237
A:Molecule type: DNA
A:Residues: 1-114 <NOZ>
A:Cross-references: UNIPROT:P25142; EMBL:X57932; NID:g38094; PIDN:CAA1003.1; PID:g82915
A:Note: the authors translated the codon ACT for residue 54 as TTP

R:Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.
Genomics 9, 775-777, 1991
A:Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence bet
A:Reference number: A54663; MUID:91244325; PMID:2037304
A:Accession: A54663
A:Molecule type: mRNA
A:Residues: 1-114 <NOL>
A:Cross-references: GB:M92161; NID:g342280; PIDN:AAA36903.1; PID:g342281
C:Genetics:
A:Intons: 1/3; 37/1; 72/2
C:Superfamily: seminal plasma protein
F:1-20/Domain: signal sequence #status predicted <SIG>

Query Match 24.4%; Score 11; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNKHPINS 30
|||||
DB 40 DLKGNKHPINS 50

RESULT 4
AF0776
conserved hypothetical protein STY2382 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AF0776
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-93 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02532.1; PID:g16503393; GSPDB:GN00176
C:Genetics:
A:Gene: STY2382

Query Match 15.6%; Score 7; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPGDSTR 16
|||||
DB 79 VPGDSTR 85

RESULT 5
D70806
probable fadD17 protein - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: D70806
R:Coile, S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70806
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-502 <COL>
A:Cross-references: UNIPROT:O53551; GB:AL022022; GB:AL123456; NID:g3261554; PIDN:CAA1774;
A:Experimental source: strain H37RV
C:Genetics:

A:Gene: fadD17
A:Accession: 4-coumarate-CoA ligase; acetate-CoA ligase homology
F:51-466/Domains: acetate-CoA ligase homology <AC1>

Query Match 15.6%; Score 7; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NEGVPGD 13
DB 272 NEGVPGD 278

RESULT 6

S41663
beta-microseminoprotein - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S41663

R:Finlund, P.; Granberg, L. B.; Roepstorff, P.

Arch. Biochem. Biophys. 309, 70-76, 1994
A:Title: Amino acid sequence of beta-microseminoprotein from porcine seminal plasma.
A:Reference number: S41663; PMID:94161559; PMID:8117114

A:Accession: S41663
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-91 <PER>
C:Superfamily: seminal plasma protein

Query Match 13.3%; Score 6; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CYFIPN 7
DB 2 CYFIPN 7

RESULT 7

PC4046
hypothetical 105 protein - Pseudomonas putida (fragment)

C:Species: Pseudomonas putida

C:Date: 04-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C:Accession: PC4046

R:Imoue, H.; Inagaki, K.; Sugimoto, M.; Esaki, N.; Soda, K.; Tanaka, H.

J. Biochem. 117, 1120-1125, 1995

A:Title: Structural analysis of the L-methionine gamma-lyase gene from Pseudomonas putida

A:Reference number: J04174; PMID:96172583; PMID:8566629

A:Accession: PC4046

A:Molecule type: DNA

A:Residues: 1-105 <INO>

A:Cross-references: UNIPROT:Q52097; GB:D8654; DDBJ:D30039; NID:91813427; PIDN:BA13643.

C:Comment: This protein shows homology with pyruvate dehydrogenase (lipoamide), and may

C:Superfamily: pyruvate dehydrogenase (lipoamide); thiamin pyrophosphate-binding domain

Query Match 13.3%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GVPGDS 14
DB 12 GVPGDS 17

RESULT 8

H86662
thiol peroxidase (EC 1.11.1.-) [imported] - Lactococcus lactis subsp. lactis (strain IL1)

C:Species: Lactococcus lactis subsp. lactis

C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C:Accession: H86662

R:Boletijn, A.; Wincker, P.; Manger, S.; Tallon, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s8

A:Reference number: A86625; PMID:21235186; PMID:11337471

A:Accession: H86662

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-160 <STO>

A:Cross-references: UNIPROT:Q9C1Q2; GB:AE005176; PID:q12723168; PIDN:AAK04402.1; GSPDB:G

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: tpx

C:Superfamily: thioredoxin peroxidase

C:Keywords: oxidoreductase

Query Match 13.3%; Score 6; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 20 DLKGNK 25
DB 30 DLKGNK 35

RESULT 9

T41423
hypothetical protein SPCC576.13 - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T41423

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21954

A:Accession: T41423

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-215 <WOO>

A:Cross-references: UNIPROT:O74897; EMBL:AL031798; PIDN:CAA21192.1; GSPDB:GN00068; SPDB:

A:Experimental source: strain 972h-; cosmid c576

C:Genetics:

A:Gene: SPDB:SPCC576.13

A:Map position: 3

Query Match 13.3%; Score 6; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 VPGDST 15
DB 20 VPGDST 25

RESULT 10

T49719
hypothetical protein B23L21.320 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C:Accession: T49719

R:Schulte, U.; Altm, V.; Hobeisel, J.; Brandt, P.; Fattmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49719

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-226 <SCH>

A:Cross-references: EMBL:AJ356172; GSPDB:GN00116; NCSP:B23L21.320

A:Experimental source: BAC clone B23L21; strain OR74A

C:Genetics:

A:Gene: NCSP:B23L21.320

A:Map position: 6

A:Inserts: 90/1

C:Superfamily: Neurospora crassa hypothetical protein B23L21.320

Query Match 13.3%; Score 6; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GVPGDS 14
 DB 134 GVPGDS 139

RESULT 11

D71187
 probable ribosomal protein L2 - *Pyrococcus horikoshii*
 C/Species: *Pyrococcus horikoshii*
 C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C/Accession: D71187
 R/Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A/Reference number: A71000; MUID:98344137; PMID:9679194
 A/Accession: D71187
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-239 <RAW>
 A/Cross-references: UNIPROT:Q59421; GB:AP000007; NID:G3236134; PIDN:BAA30891.1; PID:G325
 A/Experimental source: strain OT3
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C/Genetics:
 A/Gene: PH1775

Query Match 13.3%; Score 6; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 EGVPGD 13
 DB 112 EGVPGD 117

RESULT 12

AF1279
 hypothetical protein lmo1638 [imported] - *Listeria monocytogenes* (strain EGD-e)
 C/Species: *Listeria monocytogenes*
 C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C/Accession: AF1279
 R/Glaeser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karsst, U. Science 294, 849-852, 2001
 A/Authors: Kreft, J.; Kuhn, M.; Kunze, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma, O.K.; Schluter, T.; Simoes, N.; Tillet, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A./Title: Comparative genomics of *Listeria* species.
 A/Reference number: AB1077; MUID:21537279; PMID:11679669
 A/Accession: AF1279
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-324 <GLA>
 A/Cross-references: UNIPROT:Q8Y6F6; GB:NC_003210; PIDN:CAC99716.1; PID:G16411074; GSPDB:
 A/Experimental source: strain EGD-e
 C/Genetics:
 A/Gene: lmo1638

Query Match 13.3%; Score 6; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 FIPNEG 9
 DB 182 FIPNEG 187

RESULT 13

JC7094
 nine-heme cytochrome c - *Desulfovibrio desulfuricans*
 C/Species: *Desulfovibrio desulfuricans*
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C/Accession: JC7094
 R/Saraiya, L.M.; da Costa, P.N.; Legall, J. Biochem. Biophys. Res. Commun. 262, 629-634, 1999
 A/Title: Sequencing the gene encoding *Desulfovibrio desulfuricans* ATCC 27774 nine-heme cy
 A/Reference number: JC7094; MUID:99400423; PMID:10471375
 A/Accession: JC7094
 A/Molecule type: DNA

A/Residues: 1-326 <SAR>
 A/Cross-references: UNIPROT:Q9N68; GB:AF186393; NID:G5924394; PIDN:AAS6586.1; PID:G5924
 A/Experimental source: ATCC 27774
 C/Genetics:
 A/Gene: 9Hcc
 C/Keywords: electron transfer; heme; heme binding

Query Match 13.3%; Score 6; DB 2; Length 326;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 35 DNCENC 40
 DB 75 DNCENC 80

RESULT 14

D96614
 hypothetical protein T18124.3 [imported] - *Arabidopsis thaliana*
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: D96614
 R/Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucero, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A/Reference number: AB6141; MUID:21016719; PMID:11130712
 A/Accession: D96614
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-405 <STO>
 A/Cross-references: UNIPROT:Q9CS37; GB:AE005173; NID:G11038439; PIDN:AA627776.1; GSPDB:G
 C/Genetics:
 A/Gene: T18124.3
 A/Map position: 1

Query Match 13.3%; Score 6; DB 2; Length 405;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 FGDSTR 16
 DB 388 FGDSTR 393

RESULT 15

S41593
 translation elongation factor eEF-1 alpha chain - *Ashbya gossypii*
 C/Species: *Ashbya gossypii*
 C/Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C/Accession: S41593
 R/Steiner, S.; Philippson, P. Mol. Gen. Genet. 242, 263-271, 1994
 A/Title: Sequence and promoter analysis of the highly expressed TEF gene of the filament
 A/Reference number: S41593; MUID:94150459; PMID:8107673
 A/Accession: S41593
 A/Molecule type: DNA

A/Residues: 1-458 <STE>
 A/Cross-references: UNIPROT:P41752; EMBL:X73978; NID:G456717; PIDN:CAA52157.1; PID:G45677
 C/Genetics:

A;Gene: TER
 C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
 C;Keywords: GTP binding; methylated amino acid; nucleotide binding; P-loop; protein biosynthesis
 F;8-156/Domain: translation elongation factor Tu homology <ETU>
 F;14-21/Region: nucleotide-binding motif A (P-loop)
 F;153-156/Region: GTP-binding NKXD motif
 F;30/Modified site: N6-methyllysine (Lys) #status predicted
 F;79/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
 F;336/Modified site: N6,N6-dimethyllysine (Lys) #status predicted
 F;390/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 13.3%; Score 6; DB 2; Length 458;
 Best Local Similarity 100.0%; Pred.No. 68;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EGVPGD 13
 |||||
 Db 299 EGVPGD 304

Search completed: May 4, 2005, 14:34:56
 Job time : 17.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:04:27 ; Search time 77.2364 Seconds
(without alignments)
298.351 Million cell updates/sec

Title: US-09-977-406A-88

Perfect score: 45
Sequence: 1 SCVFIPBVGVDSTRKCMD.....HPINSEWQTNCECTCYET 45

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	114	1 MSMB_HUMAN	P08118 homo sapien
2	11	24.4	114	1 MSMB_MACMU	P25142 macaca mula
3	11	24.4	114	1 MSMB_PAPAN	Q28767 papio anubi
4	11	24.4	114	1 MSPJ_SAGO	O97949 saginus oe
5	8	17.8	112	1 MSPA_SAGO	O97936 saginus oe
6	8	17.8	114	1 MSPA_SAGO	O97935 saginus oe
7	7	15.6	93	2 O8XFD6	O8XFD6 salmone
8	7	15.6	93	2 Q7CQ92	Q7CQ92 salmone
9	7	15.6	186	2 O64859	O64859 human adeno
10	7	15.6	211	1 V33P_ADE40	P11805 human adeno
11	7	15.6	430	2 O6RS17	O6RS17 saecophaga
12	7	15.6	447	2 O6LMU9	O6LMU9 methanococ
13	7	15.6	494	2 O9VWP1	O9VWP1 drosophila
14	7	15.6	502	2 Q7DSE1	Q7DSE1 mycobacteri
15	7	15.6	502	2 O53551	O53551 mycobacteri
16	7	15.6	502	2 Q7WC5	Q7WC5 mycobacteri
17	7	15.6	758	2 Q26125	Q26125 plasmodium
18	7	15.6	759	2 Q26128	Q26128 plasmodium
19	6	13.3	40	2 O9TXA3	O9TXA3 caenorhdbi
20	6	13.3	83	2 O9S581	O9S581 drosophila
21	6	13.3	96	2 O8XW65	O8XW65 ralsconla b
22	6	13.3	97	2 O7YVW3	O7YVW3 caenorhdbi
23	6	13.3	99	2 O6YR3	O6YR3 onion yello
24	6	13.3	105	2 O52097	O52097 pseudomonas
25	6	13.3	111	2 MSMB_PIG	O02826 sus scrofa
26	6	13.3	143	2 O6K8Y1	O6K8Y1 ozyza sativ
27	6	13.3	143	2 O88AB7	O88AB7 pseudomonas
28	6	13.3	146	2 O86DE9	O86DE9 heterodera
29	6	13.3	151	2 O6FAC0	O6FAC0 acinetobact
30	6	13.3	159	1 Y000_CLOPE	O9xh85 clostridium
31	6	13.3	160	2 O9CIG2	O9CIG2 lactococcus

ALIGNMENTS

RESULT 1	ID	MSMB_HUMAN	STANDARD	PRT	114 AA.
AC	P08118	P11999	Q13125	Q9UC59	
DT	01-AUG-1988	(Rel. 08, Created)			
DT	01-AUG-1988	(Rel. 08, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).				
GN	Name=MSMB; Synonyms=PRSP;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=87161231; PubMed=3829886;				
RA	Molloy M., Nolet S., Fournier S., Benjannet S., Chapelaine P., Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidan N.G., Chretien M.,				
RT	"Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma protein secreted by the human prostate.";				
RL	DNA 6:23-29(1987).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91274357; PubMed=2054385; DOI=10.1016/0167-4781(91)90016-F;				
RA	Nolet S., Molloy M., Chretien M.,				
RT	"Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";				
RL	Biochim. Biophys. Acta 1089:247-249(1991).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90211299; PubMed=2322265;				
RA	Green C.B., Liu W.Y., Kwok S.C.M.,				
RT	"Cloning and nucleotide sequence analysis of the human beta-microseminoprotein gene.";				
RL	Biochem. Biophys. Res. Commun. 167:1184-1190(1990).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90073664; PubMed=2590204;				
RA	Uysbeck M., Lindstrom C., Weiber H., Abrahamsson P.-A., Lilja H., Lundwall A.,				
RT	"Molecular cloning of a small prostate protein, known as beta-microseminoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in non-genital tissues.";				
RL	Biochem. Biophys. Res. Commun. 164:1310-1315(1989).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	TISUS=Prostate;				
RX	MEDLINE=94115955; PubMed=7506990; DOI=10.1016/0304-3835(93)90049-F;				
RA	Liu A.Y., Bradner R.C., Vessella R.L.,				
RT	"Decreased expression of prostatic secretory protein PSP94 in prostate cancer.";				

32	6	13.3	180	2	O6G855	O6G855 uncultured
33	6	13.3	185	2	O86TZ5	O86TZ5 homo sapien
34	6	13.3	185	2	O81TJ2	O81TJ2 heterodera
35	6	13.3	189	2	O74J19	O74J19 lactobacilli
36	6	13.3	196	2	O9D8Y1	O9D8Y1 mus musculu
37	6	13.3	198	2	O6ZM71	O6ZM71 homo sapien
38	6	13.3	215	2	O74897	O74897 echinosacch
39	6	13.3	219	2	O91151	O91151 notophthalm
40	6	13.3	223	1	EMBP_MOUSE	O61878 mus musculu
41	6	13.3	225	2	O6XW07	O6XW07 shigella fl
42	6	13.3	232	2	O6JW5	O6JW5 hypocrea pa
43	6	13.3	232	2	O6JW8	O6JW8 hypocrea vi
44	6	13.3	232	2	O6JW9	O6JW9 hypocrea th
45	6	13.3	232	2	O6JXK0	O6JXK0 hypocrea th

RN [6] Cancer Lett. 74:91-99(1993).
 RN [6] SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RP TISSUE=Prostate;
 RC MEDLINE=96032566; PubMed=7566962;
 RX Xuan J.W., Chin J.L., Guo Y., Chambers A.F., Finkelman M.A.,
 RA Clarke M.W.,
 RT "Alternative splicing of PSP94 (prostatic secretory protein of 94
 RT amino acids) mRNA in prostate tissue.",
 RL Oncogene 11:1041-1047(1995).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Bajjal-Gupta M., Clarke M.W.;
 RT "Prostate specific protein (PSP94) expression in a human endometrial
 RT cell line (KLE).";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wamner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buecwo K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Dapchenko L., Mannsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.T.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguellaano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodegryn B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buttefield J.S.N., Krzywicki M.J., Skalska U., Smalls D.E.,
 RA Schmeckel A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 2-72 FROM N.A.
 RX MEDLINE=99421644; PubMed=10491085;
 RA Maekinen M., Valtonen-Andre C., Lindwall A.;
 RA Aitvama K., Yoshida Y., Schmid K., Offner G.D., Troxler R.F.,
 RA Tada R., Hara M.;
 RT "The amino acid sequence of human beta-microseminoprotein.",
 RL Biochim. Biophys. Acta 829:288-294(1995).
 RN [11]
 RP SEQUENCE OF 21-114.
 RX MEDLINE=55004133; PubMed=6434350; DOI=10.1016/0014-5793(84)80766-8;
 RA Seidah N.G., Abbatini N.U., Rochement Y., Sheth A., Chretien M.;
 RT "Complete amino acid sequence of human seminal plasma beta-inhibin.
 RT Prediction of post Gln-Arg cleavage as a maturation site.",
 RL FEBS Lett. 175:349-355(1984).
 RN [12]
 RP SEQUENCE OF 21-50 AND 113-114.
 RX MEDLINE=92028964; PubMed=1930232;
 RA Liang Z.G., Kamada M., Koide S.S.;
 RT "Structural identity of immunoglobulin binding factor and prostatic
 RT secretory protein of human seminal plasma.",
 RL Biochem. Biophys. Res. Commun. 180:356-359(1991).
 RN [13]
 RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.
 RC TISSUE=Semen;
 RX MEDLINE=95401076; PubMed=7671139; DOI=10.1016/1357-2725(95)00021-G;
 RA Ohkubo I., Tada T., Ochiat Y., Ueyama H., Himoto T., Sasaki M.;

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RT      "Human seminal plasma beta-microseminoprotein: its purification,
RT      characterization, and immunohistochemical localization.",
RT      Int. J. Biochem. Cell Biol. 27:603-611(1995).
RN      [14]
RP      SEQUENCE OF 21-32.
RX      MEDLINE=21648993; PubMed=11788998;
RX      DOI=10.1002/1615-9861(200201)2:1<112::AID-PROT112>3.CO;2-E;
RA      Ghafoori B., Stahlbow B., Tagesson C., Lindahl M.;
RA      "Newly identified proteins in human nasal lavage fluid from non-
RT      smokers and smokers using two-dimensional gel electrophoresis and
RT      peptide mass fingerprinting.",
RL      Proteomics 2:112-120(2002).
CC      -1- SUBCELLULAR LOCATION: Secreted. Sperm surface.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named Isoforms=2;
CC      Name=PSp94;
CC      IsoId=P08118-1; Sequence=Displayed;
CC      Name=PSp57;
CC      IsoId=P08118-2; Sequence=VSP_003275, VSP_003276;
CC      -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,
CC      breast and penis. Also expressed in pancreas, esophagus, stomach,
CC      duodenum, colon, trachea, lung, salivary glands and fallopian
CC      tube. PSp94 is expressed in lung and breast, whereas PSp57 is
CC      found in kidney and bladder.
CC      -1- MISCELLANEOUS: Specific receptors for this protein are found on
CC      spermatozoa and in the prostate.
CC      -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC      CAUTION: Was originally thought to inhibit the secretion of FSH by
CC      pituitary cells.
CC      -----
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CC      or send an email to license@ebi.ac.uk).
CC      -----
DR      EMBL, M34376; AAAS9871.1; -.
DR      EMBL, M34373; AAAS9871.1; JOINED.
DR      EMBL, M34374; AAAS9871.1; JOINED.
DR      EMBL, M34375; AAAS9871.1; JOINED.
DR      EMBL, M15885; AAAS6533.1; -.
DR      EMBL, X57928; CAA41002.1; -.
DR      EMBL, X57929; CAA41002.1; JOINED.
DR      EMBL, X57930; CAA41002.1; JOINED.
DR      EMBL, X57931; CAA41002.1; JOINED.
DR      EMBL, S67815; AAB29732.1; -.
DR      EMBL, U22178; AAA83556.1; -.
DR      EMBL, U78976; AAB37355.1; -.
DR      EMBL, BC005257; AAH05257.1; -.
DR      EMBL, AJ133356; CAB39325.1; -.
DR      PIR, A34567; A34567.
DR      PIR, G01730; G01730.
DR      Genew, HGNC:7372; MSMB.
DR      H-InvDB, HIX0008822; -.
DR      MIM, 157145; -.
DR      GO, GO:0005615; C:extracellular space; TAS.
DR      GO, GO:0005634; C:nucleus; TAS.
DR      InterPro, IPR008735; PSp94.
DR      Pfam, PF05825; PSp94; 1.
KW      Alternative splicing; Direct protein sequencing; Polymorphism; Signal.
FT      SIGNAL 1 20
FT      CHAIN 21 114 Beta-microseminoprotein.
FT      DISULFID 22 38 By similarity.
FT      DISULFID 37 93 By similarity.
FT      DISULFID 60 69 Or C-60 with C-70 (By similarity).
FT      DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT      DISULFID 84 107 By similarity.
FT      VARSPIC 37 77 KMDIDGNKHPISEMOTGNCCTCYETGISCTLTSTPV
FT      -> MFLHWMTYTKAESRRRTASISWRRRTQKRPVLS
FT      VNG (in isoform PSp57).
FT      /FTId=VSP_003275.

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GN Name=MSPT;
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCB1_Taxid=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL; AJ010155; CAB38123.1; -.
DR EMBL; AJ010156; CAB38123.1; JOINED.
DR EMBL; AJ010157; CAB38123.1; JOINED.
DR GO; GO:0005576; C:extracellular; NAS.
DR InterPro; IPR008735; PSp94.
DR Pfam; PF05825; PSp94; 1.
KW Signal.
FT CHAIN 1 20 Potential.
FT SIGNAL 21 114 Beta-microseminoprotein J1.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.
FT DISULFID 60 63 Or C-60 with C-70 (By similarity).
FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT DISULFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 12746 MW; F3F05B013445BAD4 CRC64;

Query Match 24.4%; Score 11; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNKHPINS 30
DB 40 DLKGNKHPINS 50

RESULT 5
MSPE_SAGOE STANDARD; PRT; 112 AA.
AC 097936;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein A1 precursor (msp-A1) (Fragment).
GN Name=MSPA;
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCB1_Taxid=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
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CC -----
DR EMBL; AJ010158; CAB38124.1; -.
DR EMBL; AJ010159; CAB38124.1; JOINED.
DR GO; GO:0005576; C:extracellular; TAS.
DR InterPro; IPR002400; GF_cyskn0t.
DR InterPro; IPR008735; PSp94.
DR Pfam; PF05825; PSp94; 1.
DR PRINTS; PR00438; GFCYSKN0T.
KW Signal.
FT NON_TER 1 19 By similarity.
FT SIGNAL <1 19 Beta-microseminoprotein A1.
FT CHAIN 20 112 By similarity.
FT DISULFID 21 37 By similarity.
FT DISULFID 56 92 By similarity.
FT DISULFID 59 68 Or C-59 with C-69 (By similarity).
FT DISULFID 61 69 Or C-61 with C-68 (By similarity).
FT DISULFID 83 106 By similarity.
SQ SEQUENCE 112 AA; 12631 MW; DDA06BFC1C5CD79B CRC64;

Query Match 17.8%; Score 8; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.91;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNKHP 27
DB 39 DLKGNKHP 46

RESULT 6
MSPE_SAGOE STANDARD; PRT; 114 AA.
AC 097935;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein E1 precursor (msp-E1).
GN Name=MSPE;
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCB1_Taxid=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99421644; PubMed=10491085;
RA Maekinen M., Valtanen-Andre C., Lundwall A.;
RT "New world, but not old world, monkeys carry several genes encoding
beta-microseminoprotein."
RL Eur. J. Biochem. 264:407-414(1999).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC -----
DR EMBL; AJ010154; CAB38105.1; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR InterPro; IPR008735; PSp94.
DR Pfam; PF05825; PSp94; 1.
KW Signal.
FT CHAIN 1 20 Potential.
FT SIGNAL 21 114 Beta-microseminoprotein E1.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.

```


FT DISULFID 60 69 Or C-60 with C-70 (By similarity).
 FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
 FT DISULFID 84 107 By similarity.
 SQ SEQUENCE 114 AA; 12738 MW; 05E7A410125C94B2 CRC64;

Query Match 17.8%; Score 8; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.92;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DLKGNKAP 27
 DB 40 DLKGNKAP 47

RESULT 7

08XFD6 PRELIMINARY; PRT; 93 AA.
 ID 08XFD6; 07AM07;
 AC 08XFD6; 07AM07;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Hypothetical protein yehf (Hypothetical protein STY2382).
 GN Name=yehf; OrderedLocNames=STY2382, t0703;
 OS Salmoneilla typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmoneilla.
 NC NCB1_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.,
 RT "Comparative genomics of Salmoneilla enterica serovar Typhi strains Ty2
 and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell A., Harlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogg A., Larsen T.S., Leach S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrrell B.G.,
 RT "Complete genome sequence of a multiple drug resistant Salmoneilla
 enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL; ABO16836; AAO68400.1; -;
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 93 AA; 9929 MW; B2FCE9D9F079EE98 CRC64;

Query Match 15.6%; Score 7; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPGDSTR 16
 DB 79 VPGDSTR 85

RESULT 8

07CQ92 PRELIMINARY; PRT; 93 AA.
 AC 07CQ92;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)

DE Putative outer membrane protein.
 GN Name=yehf; OrderedLocNames=STM2153;
 OS Salmoneilla typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmoneilla.
 NC NCB1_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.,
 RT "Complete genome sequence of Salmoneilla enterica serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 DR EMBL; AEO08796; AAL21056.1; -;
 KM Complete proteome.
 SQ SEQUENCE 93 AA; 9929 MW; B2FCE9D9F079EE98 CRC64;

Query Match 15.6%; Score 7; DB 2; Length 93;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VPGDSTR 16
 DB 79 VPGDSTR 85

RESULT 9

064859 PRELIMINARY; PRT; 186 AA.
 ID 064859;
 AC 064859;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Human adenovirus F.
 OS Human adenovirus F.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 NC NCB1_TaxID=130309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88084437; PubMed=2961652; DOI=10.1016/0378-1119(87)90034-5;
 RA van Loon A.E., Ligtenberg M., Reemst A.M., Sussendach J.S.,
 RA Roelijn T.H.,
 RT "Structure and organization of the left-terminal DNA regions of
 RT fastidious adenovirus types 40 and 41.";
 RL Gene 58:109-126(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88265890; PubMed=2968714;
 RA Ishino M., Ohashi Y., Emoto T., Sawada Y., Fujinaga K.,
 RT "Characterization of adenovirus type 40 E1 region.";
 RL Virology 165:95-102(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87122182; PubMed=3811242;
 RA Ishino M., Sawada Y., Yaegashi T., Demura M., Fujinaga K.,
 RT "Nucleotide sequence of the adenovirus type 40 inverted terminal
 RT repeat: close relation to that of adenovirus type 5.";
 RL Virology 156:414-416(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88160034; PubMed=3279700;
 RA Vos H.L., van der Lee F.M., Reemst A.M., van Loon A.E.,
 RA Sussendach J.S.,
 RT "The genes encoding the DNA binding protein and the 23k protease of
 RT adenovirus types 40 and 41.";
 RL Virology 163:1-10(1988).
 RN [5]
 RP SEQUENCE FROM N.A.

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RX MEDLINE=89370295; PubMed=2773314;
RA Kidd A.H., Erasmus M.J.;
RT "sequence characterization of the adenovirus 40 fiber gene.";
RL Virology 172:113-144(1989).
RN
RP SEQUENCE FROM N.A.
RA Ishino M.;
RT "Analysis of structure and function of human adenovirus type 40
RT leftmost 1.85 kb region including transforming E1A gene.";
RL Sapporo Igaku Zasshi 57:59-66(1988).
RN
RP SEQUENCE FROM N.A.
RA MEDLINE=94087748; PubMed=8263936;
RA Davidson A.J., Telford E.A., Watson M.S., McBride K., Mautner V.;
RT "The DNA sequence of adenovirus type 40.";
RL J. Mol. Biol. 234:1308-1316(1993).
RN
RP SEQUENCE FROM N.A.
RA MEDLINE=90111698; PubMed=2481711;
RA Toogood C.I., Murrall R., Burnett R.M., Hay R.T.;
RT "The adenovirus type 40 hexon: sequence, predicted structure and
RT relationship to other adenovirus hexons.";
RL J. Gen. Virol. 70:3203-3214(1989).
RN
RP SEQUENCE FROM N.A.
RA Davidson A.J., Benko M., Harrach B.;
RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: L19443; AAC13971.1;
SQ SEQUENCE 186 AA; 21302 MW; 15C19FD4B723E7B5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 186;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGNKHPI 28
DB 4 KGNKHPI 10

RESULT 10
V33P ADE40
AC P11805; STANDARD; PRT; 211 AA.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 01-FEB-1996 (Rel. 33, Last annotation update)
DE 33 kDa phosphoprotein.
OS Human adenovirus type 40.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28284;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Dugan;
RX MEDLINE=94087748; PubMed=8263936;
RA Davidson A.J., Telford E.A., Watson M.S., McBride K., Mautner V.;
RT "The DNA sequence of adenovirus type 40.";
RL J. Mol. Biol. 234:1308-1316(1993).
RN
RP SEQUENCE OF 176-211 FROM N.A.
RX MEDLINE=88160034; PubMed=3279700;
RA Vos H.L., der Lee F.M., Reemst A.M.C.B., van Loon A.E.,
RA Susenbach J.S.;
RT "The genes encoding the DNA binding protein and the 23K protease of
RT adenovirus types 40 and 41.";
RL Virology 163:1-10(1988).
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CC
DR EMBL: L19443; AAC13956.1;
DR EMBL: M19316; AAA52199.1;
KW late protein; Phosphorylation.
SQ SEQUENCE 211 AA; 24162 MW; AAD90FC8B34EB3CA CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 1; Length 211;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 KGNKHPI 28
DB 4 KGNKHPI 10

RESULT 11
Q6RS17
AC Q6RS17; PRELIMINARY; PRT; 430 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Yolk protein C.
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN
RP SEQUENCE FROM N.A.
RA Hens K., Lemey P., Macours N., Francis C., Huybrechts R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY494776; AAS75327.1;
DR GO: GO:0003824; F: catalytic activity; IEA.
DR GO: GO:0006629; P: lipid metabolism; IEA.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00151; Lipase; 1.
SQ SEQUENCE 430 AA; 47252 MW; 5A80321B157107FA CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 2; Length 430;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PNEGVPV 12
DB 329 PNEGVPV 335

RESULT 12
Q6LMU9
AC Q6LMU9; PRELIMINARY; PRT; 447 AA.
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Pyruvate kinase (EC 2.7.1.40).
GN OrderedlocusNames=MMP1605;
OS Methanococcus maripaludis.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanococcaceae; Methanococcus.
OX NCBI_TaxID=39152;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=82 / LL;
RA Hendrickson E.L., Kaul R., Zhou Y., Boyce D., Chapman P., Chung J.,
RA Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
RA Saenphimmachak C., Soll D., Whitman W.B., Latimer F.W., Olson M.V.,
RA Leigh J.A.;
RT "Complete genome sequence of the mesophilic hydrogenotrophic
RT methanogen Methanococcus maripaludis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

```

CC -1- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
 CC -1- COFACTOR: Requires magnesium and potassium (By similarity).
 CC -1- PATHWAY: Glycolysis; final step.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SIMILARITY: Belongs to the pyruvate kinase family.
 DR EMBL: BX957223; CcP1161.1; -.
 DR HSPB: P11974; IAOF.
 DR GO: GO:0004743; F:pyruvate kinase activity; IEA.
 DR GO: GO:0006096; P:glycolysis; IEA.
 DR InterPro: IPR01037; PK_B_barrel_like.
 DR InterPro: IPR01697; Pyruvate_kinase.
 DR Pfam: PF02887; PK_C; 1.
 DR Pfam: PF02887; PK_C; 1.
 DR PRINTS: PR01050; PYRUVTKINASE.
 DR PRODOM: PD001009; Pyruvate_kinase: 2.
 DR TIGRFAMs: TIGR01064; pyruv_kin; 1.
 DR PROSITE: PS00110; PYRUVATE_KINASE; UNKNOWN_1.
 KW Complete proteome; Glycolysis; Kinase; Magnesium; Transferase.
 SQ SEQUENCE 447 AA; 50143 MW; ABBB59767D54EDD6 CRC64;

Query Match 15.6%; Score 7; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 MDLKGK 25
 Db 63 MDLKGK 69

RESULT 13

09VMP1 PRELIMINARY; PRT; 494 AA.

ID 09VMP1 PRELIMINARY; PRT; 494 AA.
 AC 09VMP1; 095RE2; 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE C67288-PA (LD38070p).
 GN ORFNames=CG7288;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burks K.C., Busam D.A., Butler H., Caden E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostalka D., Houston K.H., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mates J., McIntosh T.C., McLeod M.P., McPherson S.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris A., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskens D.R., Paclob J.M.,
 RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2242605; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskaas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [13]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2242607; PubMed=12537573;
 RA Kankiner J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2242609; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kankiner J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [15]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP SEQUENCE FROM N.A.
 RX FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [17]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Munro J., Paclob J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AEO03510; AAF4897.2; -.
 DR EMBL: AY061442; ALF28990.1; -.
 DR FlyBase; FBgn0030969; CG7288.
 DR GO: GO:0004197; F:cysteine-type endopeptidase activity; IEA.
 DR GO: GO:0004221; F:ubiquitin thiolesterase activity; IEA.
 DR GO: GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
 DR InterPro: IPR001394; Peptidase_C19.
 DR Pfam: PF00443; UCH; 1.
 DR PROSITE: PSS0235; UCH 2.3; 1.
 SQ SEQUENCE 494 AA; 57503 MW; D7C9B515BC8397 CRC64;

Query Match 15.6%; Score 7; DB 2; Length 494;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LKGNKHP 27
 DB 268 LKGNKHP 274

RESULT 14

Q7D5E1 PRELIMINARY; PRT; 502 AA.
 ID Q7D5E1;
 AC Q7D5E1;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE 4-coumarate-CoA ligase, putative.
 GN OrderedLocustNames=MT3610;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RX DOI=10.1128/JB.184.19.5479-5490.2002;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.D., Debay R.T., Dodson R.J., Gwin M.L., Haft D.H.,
 RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ertolaeva M.D.,
 RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
 RA Gill J., Minkula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
 RA Fraser C.M.;
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL J. Bacteriol. 184:5479-5490(2002).
 CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 CC family.
 CC EMBL; AE000516; AAK47969.1; -.
 DR TIGR; MT3610; -.
 DR GO; GO:0016874; F.ligase activity; IEA.
 DR GO; GO:0008152; Pimicabolism; IEA.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 KM Ligase.
 SQ SEQUENCE 502 AA; 53690 MW; 0B47BC5203C28BF7 CRC64;

Query Match 15.6%; Score 7; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NEGVPD 13
 DB 272 NEGVPD 278

RESULT 15

O53551 PRELIMINARY; PRT; 502 AA.
 ID O53551;
 AC O53551;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE POSSIBLE FATTY-ACID-CoA SYNTHETASE FADD17 (FATTY-ACID-CoA SYNTHASE)
 DE (FATTY-ACID-CoA LIGASE) (EC 6.2.1.-).
 GN Name=fadd17; OrderedLocustNames=RV3506;
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OC NCBI_TaxID=1773;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37Rv;
 RX MEDLINE=98295987; PubMed=9634230; DOI=10.1038/31159;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C.M.,
 RA Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III,
 RA Tekala F., Badcock K., Basham D., Brown D., Chillingworth T.,
 RA Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S.,
 RA Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A.,
 RA Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 CC -1- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
 CC family.
 CC EMBL; BX842583; CA117743.1; -.
 DR PIR; D70806; D70806.
 DR HSSP; P08659; ILCT.
 DR Tuberculist; RV3506; -.
 DR GO; GO:0016874; F.ligase activity; IEA.
 DR GO; GO:0008152; Pimicabolism; IEA.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF00501; AMP-binding; 1.
 DR PRINTS; PR00154; AMPBINDING.
 DR PROSITE; PS00455; AMP_BINDING; 1.
 KM Complete proteome; Ligase.
 SQ SEQUENCE 502 AA; 53738 MW; 0AF9A7B3B9C83A4D CRC64;

Query Match 15.6%; Score 7; DB 2; Length 502;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NEGVPD 13
 DB 272 NEGVPD 278

Search completed: May 4, 2005, 14:33:12
 Job time : 79.2364 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:03:32 ; Search time 60.6545 Seconds
(without alignments)
191.293 Million cell updates/sec

Title: US-09-977-406A-90

Perfect score: 30

Sequence: 1 EMQTDNCETCTCYETEMQTDNCETCTCYET 30

Scoring table: OLIGO

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	AAO17997	AAO17997 Human PSP
2	30	100.0	45	AAO17998	AAO17998 Human PSP
3	30	100.0	60	AAO17999	AAO17999 Human PSP
4	16	53.3	16	AAO17917	AAO17917 Human pro
5	16	53.3	17	AAO17918	AAO17918 Human pro
6	16	53.3	18	AAO17919	AAO17919 Human pro
7	16	53.3	19	AAO17920	AAO17920 Human pro
8	16	53.3	20	AAO17921	AAO17921 Human pro
9	16	53.3	21	AAO17922	AAO17922 Human pro
10	16	53.3	22	AAO17923	AAO17923 Human pro
11	16	53.3	23	AAO17924	AAO17924 Human pro
12	16	53.3	24	AAO17925	AAO17925 Human pro
13	16	53.3	25	AAO17926	AAO17926 Human pro
14	16	53.3	26	AAO17927	AAO17927 Human pro
15	16	53.3	27	AAO17928	AAO17928 Human pro
16	16	53.3	28	AAO17929	AAO17929 Human pro
17	16	53.3	29	AAO17930	AAO17930 Human pro
18	16	53.3	30	AAO17931	AAO17931 Human pro
19	16	53.3	31	AAO17932	AAO17932 Human pro
20	16	53.3	32	AAO17933	AAO17933 Human pro
21	16	53.3	33	AAO17934	AAO17934 Human pro
22	16	53.3	34	AAO17935	AAO17935 Human pro
23	16	53.3	35	AAO17936	AAO17936 Human pro
24	16	53.3	36	AAO17937	AAO17937 Human pro
25	16	53.3	37	AAO17938	AAO17938 Human pro

26	16	53.3	38	AAO17939	AAO17939 Human pro
27	16	53.3	39	AAO17940	AAO17940 Human pro
28	16	53.3	40	AAO17941	AAO17941 Human pro
29	16	53.3	41	AAO17942	AAO17942 Human pro
30	16	53.3	42	AAO17943	AAO17943 Human pro
31	16	53.3	43	AAO17944	AAO17944 Human pro
32	16	53.3	44	AAO17945	AAO17945 Human pro
33	16	53.3	45	AAO17946	AAO17946 Human pro
34	16	53.3	46	AAO17947	AAO17947 Human pro
35	16	53.3	47	AAO17948	AAO17948 Human pro
36	16	53.3	48	AAO17949	AAO17949 Human pro
37	16	53.3	49	AAO17950	AAO17950 Human pro
38	16	53.3	50	AAO17951	AAO17951 Human pro
39	16	53.3	51	AAO17952	AAO17952 Human pro
40	16	53.3	52	AAO17953	AAO17953 Human pro
41	16	53.3	53	AAO17954	AAO17954 Human pro
42	16	53.3	54	AAO17955	AAO17955 Human pro
43	16	53.3	55	AAO17956	AAO17956 Human pro
44	16	53.3	56	AAO17957	AAO17957 Human pro
45	16	53.3	57	AAO17958	AAO17958 Human pro

ALIGNMENTS

RESULT 1
ID AAO17997 standard; peptide, 30 AA.

AAO17997;

30-AUG-2002 (first entry)

Human PSP94 analogue adaptor peptide #1.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-nucleosinoprotein; human seminal plasma inhibin; analogue;

prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

benign prostate hyperplasia; cytostatic.

Synthetic.

WO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PRO-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Disclousure; Page 105; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of PSH. The

present sequence is an adaptor peptide useful in the invention

XX
SQ Sequence 30 AA;
Query Match 100.0%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
DB 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
RESULT 2
AAO17998
ID AAO17998 standard; protein; 45 AA.
XX
AC AAO17998;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human PSP94 analogue adaptor peptide #2.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
OS Synthetic.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
DR WPI; 2002-471401/50.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001MO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
DR WPI; 2002-471401/50.
XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Disclosure; Page 106; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an adaptor peptide useful in the invention
XX
SQ Sequence 45 AA;
Query Match 100.0%; Score 30; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
DB 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
RESULT 3

AAO17999
ID AAO17999 standard; protein; 60 AA.
XX
AC AAO17999;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human PSP94 analogue adaptor peptide #3.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
OS Synthetic.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
DR WPI; 2002-471401/50.
XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Disclosure; Page 106; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumors, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an adaptor peptide useful in the invention
XX
SQ Sequence 60 AA;
Query Match 100.0%; Score 30; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
DB 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
RESULT 4
AAO17917
ID AAO17917 standard; peptide; 16 AA.
XX
AC AAO17917;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #6.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

KM benign prostate hyperplasia; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200233090-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 76; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 16 AA;
XX
Query Match 53.3%; Score 16; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EMQTDNCETCTCYETE 16
Db |||||
1 EMQTDNCETCTCYETE 16
XX
RESULT 5
AAOI7918
ID AAO17918 standard; peptide; 17 AA.
XX
AC AAO17918;
XX
XX 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #7.
XX
XX
KM Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
KM beta-microseminoprotein; human seminal plasma inhibin; analogue;
KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KM benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200233090-A2.
XX
PN 25-APR-2002.
XX
PD 15-OCT-2001; 2001WO-CA001463.
XX
PF 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX

PA (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 76; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 17 AA;
XX
Query Match 53.3%; Score 16; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 EMQTDNCETCTCYETE 16
Db |||||
1 EMQTDNCETCTCYETE 16
XX
RESULT 6
AAOI7919
ID AAO17919 standard; peptide; 18 AA.
XX
AC AAO17919;
XX
XX 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #8.
XX
XX
KM Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
KM beta-microseminoprotein; human seminal plasma inhibin; analogue;
KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KM benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200233090-A2.
XX
PN 25-APR-2002.
XX
PD 15-OCT-2001; 2001WO-CA001463.
XX
PF 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 77; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate

CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminalprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostatic hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX

XX Sequence 18 AA;

Query Match 53.3%; Score 16; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.3e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYETE 16
 Db 1 EWQTDNCETCTCYETE 16

RESULT 7

ID AAO17920 standard; peptide; 19 AA.

XX AAO17920;

DT 30-AUG-2002 (first entry)

DE Human prostatic secretory protein of 94 amino acids PSP94 analogue #9.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminalprotein; human seminal plasma inhibin; analogue;
 KM prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
 XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostatic hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostatic secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 77; 185pp; English.

XX The present invention relates to analogues of the human prostatic
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminalprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostatic hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX

XX Sequence 19 AA;

Query Match 53.3%; Score 16; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.5e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYETE 16
 Db 1 EWQTDNCETCTCYETE 16

RESULT 8

ID AAO17921 standard; peptide; 20 AA.

XX AAO17921;

DT 30-AUG-2002 (first entry)

DE Human prostatic secretory protein of 94 amino acids PSP94 analogue #10.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KW beta-microseminalprotein; human seminal plasma inhibin; analogue;
 KM prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostatic hyperplasia; cytostatic.

XX Homo sapiens.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostatic secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 77; 185pp; English.

XX The present invention relates to analogues of the human prostatic
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microseminalprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostatic hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 XX

XX Sequence 20 AA;

Query Match 53.3%; Score 16; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.7e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EWQTDNCETCTCYETE 16
 Db 1 EWQTDNCETCTCYETE 16

RESULT 9

ID AAO17922 standard; peptide; 21 AA.

XX AAO17922;

DT 30-AUG-2002 (first entry)
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #11.
DE
XX
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
OS Homo sapiens.
XX
XX WO200233090-A2.
XX
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-CA001463.
XX
XX 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 78; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
XX
XX Sequence 21 AA;
SQ
Query Match 53.3%; Score 16; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16
RESULT 10
AA017923 standard; peptide; 22 AA.
ID AA017923
XX
XX AA017923;
XX
XX 30-AUG-2002 (first entry)
XX
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #12.
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
OS Homo sapiens.
XX
XX WO200233090-A2.
XX
XX

XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-CA001463.
XX
XX 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 78; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
XX secretory protein of 94 amino acids (PSP94, also known as prostatic
XX inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
XX microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
XX growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
XX cancer, breast cancer, endometrial, ovarian or other cancers of
XX epithelial secretion, or benign prostate hyperplasia and for treating
XX patients with a disease characterized by elevated levels of FSH. The
XX present sequence is an analogue of the invention
XX
XX Sequence 22 AA;
SQ
Query Match 53.3%; Score 16; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16
RESULT 11
AA017924 standard; peptide; 23 AA.
ID AA017924
XX
XX AA017924;
XX
XX 30-AUG-2002 (first entry)
XX
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #13.
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
XX beta-microseminoprotein; human seminal plasma inhibin; analogue;
XX prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
XX stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
XX benign prostate hyperplasia; cytostatic.
OS Homo sapiens.
XX
XX WO200233090-A2.
XX
XX 25-APR-2002.
XX
XX 15-OCT-2001; 2001WO-CA001463.
XX
XX 16-OCT-2000; 2000CA-02321256.
XX 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
XX
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
XX

RESULT 14

AA017927 standard; peptide; 26 AA.

AA017927;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94 analogue #16.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-microseminoprotein; human seminal plasma inhibin; analogue;

prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

benign prostate hyperplasia; cytostatic.

Homo sapiens.

WO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 79; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP)). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 26 AA;

Query Match 53.3%; Score 16; DB 5; Length 26;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.

Homo sapiens.

WO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 79; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP)). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 27 AA;

Query Match 53.3%; Score 16; DB 5; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.8e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

1 EWQTDNCETCTCYETE 16

Search completed: May 4, 2005, 14:25:11

Job time : 60.6545 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:13:33 ; Search time 15.3818 Seconds

(without alignment)
145.592 Million cell updates/sec

Title: US-09-977-406A-90

Perfect score: 30

Sequence: 1 EMQDNCETCTCYETEMQDNCETCTCYET 30

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	53.3	94	US-07-899-535A-1	Sequence 1, Appli
2	16	53.3	114	US-09-513-999C-7807	Sequence 7807, Ap
3	6	20.0	241	US-08-460-309-17	Sequence 17, Appl
4	6	20.0	241	US-08-125-077-17	Sequence 17, Appl
5	6	20.0	362	US-09-248-796A-20514	Sequence 20514, A
6	6	20.0	2123	US-09-949-016-7517	Sequence 7517, Ap
7	6	20.0	3070	US-09-561-403-7	Sequence 7, Appli
8	6	20.0	3088	US-09-562-702A-8	Sequence 8, Appli
9	6	20.0	3089	US-09-562-702A-4	Sequence 4, Appli
10	6	20.0	3110	US-09-562-702A-2	Sequence 2, Appli
11	6	20.0	3110	US-09-562-702A-6	Sequence 6, Appli
12	6	20.0	3110	US-09-561-709B-7	Sequence 7, Appli
13	6	20.0	3110	US-09-917-254-86	Sequence 86, Appli
14	6	20.0	3110	US-09-949-016-5937	Sequence 5937, Ap
15	6	20.0	3111	US-08-460-309-4	Sequence 4, Appli
16	6	20.0	3111	US-08-125-077-4	Sequence 4, Appli
17	5	16.7	9	US-08-481-968A-24	Sequence 24, Appl
18	5	16.7	9	US-08-154-712B-24	Sequence 24, Appl
19	5	16.7	9	US-09-947-925A-24	Sequence 24, Appl
20	5	16.7	37	US-09-917-340-57	Sequence 57, Appl
21	5	16.7	37	US-09-829-481-11	Sequence 11, Appl
22	5	16.7	38	US-09-030-619-199	Sequence 199, App
23	5	16.7	38	US-09-030-619-200	Sequence 200, App
24	5	16.7	58	US-09-621-976-5440	Sequence 5440, Ap
25	5	16.7	75	US-09-107-532A-4113	Sequence 4113, Ap
26	5	16.7	104	US-09-621-976-6750	Sequence 6750, Ap
27	5	16.7	107	US-09-513-999C-7986	Sequence 7986, Ap

28	5	16.7	110	US-09-513-999C-7055	Sequence 7055, Ap
29	5	16.7	188	US-09-270-767-61692	Sequence 61692, A
30	5	16.7	192	US-08-685-466C-4	Sequence 4, Appli
31	5	16.7	230	US-09-248-796A-21826	Sequence 21826, A
32	5	16.7	231	US-09-265-540E-4	Sequence 4, Appli
33	5	16.7	243	US-08-460-309-15	Sequence 15, Appl
34	5	16.7	243	US-08-460-309-16	Sequence 16, Appl
35	5	16.7	243	US-08-125-077-15	Sequence 15, Appl
36	5	16.7	243	US-08-125-077-16	Sequence 16, Appl
37	5	16.7	259	US-09-328-352-5038	Sequence 5038, Ap
38	5	16.7	261	US-09-962-357-8	Sequence 8, Appli
39	5	16.7	314	US-08-486-036A-4	Sequence 4, Appli
40	5	16.7	314	US-09-005-298-4	Sequence 4, Appli
41	5	16.7	314	US-08-768-619-4	Sequence 4, Appli
42	5	16.7	314	PCT-US96-09848-4	Sequence 4, Appli
43	5	16.7	315	US-09-902-540-14527	Sequence 14527, A
44	5	16.7	316	US-08-482-282B-4	Sequence 4, Appli
45	5	16.7	316	US-09-543-681A-5873	Sequence 5873, Ap

ALIGNMENTS

RESULT 1
US-07-899-535A-1
Sequence 1, Application US/07899535A
Patent No. 5428011
GENERAL INFORMATION:
APPLICANT: Sheeh, Anil R.
APPLICANT: Garde, Seema
APPLICANT: Panchal, Chandra J.
TITLE OF INVENTION: Pharmaceutical Preparations For
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Mr. George Loud
STREET: 2001 Jefferson Davis Highway, Suite 306
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,535A
FILING DATE: 16-JUN-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Loud, George A.
REGISTRATION NUMBER: 25,814
REFERENCE/DOCKET NUMBER: SGB-A835
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-0960
TELEFAX: 703-415-0962
TELEX: 24 8614
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-07-899-535A-1
Query Match 53.3%; Score 16; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 76-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||||
Db 31 EMQDNCETCTCYETE 46

RESULT 2
US-09-513-999C-7807
; Sequence 7807, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7807
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; OTHER INFORMATION: score 9
; OTHER INFORMATION: seq VVFATFVTLGNA/SC
US-09-513-999C-7807

Query Match 53.3%; Score 16; DB 4; Length 114;
Best Local Similarity 100.0%; Pred.No. 8.4e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
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Db 51 EMQDNCETCTCYETE 66

RESULT 3
US-08-460-309-17
; Sequence 17, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994

/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/472,319
/ FILING DATE: 30-JAN-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/919,951
/ FILING DATE: 27-JUL-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-LA 9721
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 241 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
US-08-460-309-17

Query Match 20.0%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred.No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
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Db 103 NCETCT 108

RESULT 4
US-08-125-077-17
; Sequence 17, Application US/08125077
; Patent No. 5872231
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-LA 9721
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-17

Query Match 20.0%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 103 NCERTCT 108

RESULT 5
US-09-248-796A-20514
Sequence 20514, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Ketch Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
CURRENT APPLICATION NUMBER: US/09/248,796A
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/096,409
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20514
LENGTH: 362
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20514

Query Match 20.0%; Score 6; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TEMQTD 20
Db 341 TEMQTD 346

RESULT 6
US-09-949-016-7517
Sequence 7517, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7517
LENGTH: 2123
TYPE: PRT
ORGANISM: Human
US-09-949-016-7517

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Best Local Similarity 100.0%; Pred. No. 59;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 NCERTCT 11
Db 405 NCERTCT 410

RESULT 7
US-09-961-403-7
Sequence 7, Application US/09961403
Patent No. 6780594
GENERAL INFORMATION:

APPLICANT: HE-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KRAFT, BERTHOUT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 3070
TYPE: PRT
ORGANISM: Homo sapiens
US-09-961-403-7

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Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 8
US-09-562-702A-8
Sequence 8, Application US/09562702A
Patent No. 6632790
GENERAL INFORMATION:
APPLICANT: Yurchenco, Peter
TITLE OF INVENTION: Laminin 2 and Methods for Its Use
FILE REFERENCE: 99-274-B
CURRENT APPLICATION NUMBER: US/09/562,702A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/155,945
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 60/143,289
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/139,198
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/131,720
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 3088
TYPE: PRT
ORGANISM: Homo sapiens
US-09-562-702A-8

Query Match 20.0%; Score 6; DB 4; Length 3088;
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QY 6 NCERTCT 11
Db 367 NCERTCT 372

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RESULT 9
US-09-562-702A-4
; Sequence 4, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-4

Query Match
Best Local Similarity 20.0%; Score 6; DB 4; Length 3089;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
Db 367 NCETCT 372

RESULT 10
US-09-562-702A-2
; Sequence 2, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-2

Query Match
Best Local Similarity 20.0%; Score 6; DB 4; Length 3110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-562-702A-6
; Sequence 6, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
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; SEQ ID NO 6
; LENGTH: 3110
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; ORGANISM: Homo sapiens
US-09-562-702A-6

Query Match
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 389 NCETCT 394
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RESULT 12
US-09-561-709B-7
; Sequence 7, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgess, Robert
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-7

Query Match
Best Local Similarity 20.0%; Score 6; DB 4; Length 3110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 NCETCT 11
Db 389 NCETCT 394
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RESULT 13
US-09-917-254-86
; Sequence 86, Application US/09917254
; Patent No. 6703204
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QY 6 NCETCT 11
Db 389 NCETCT 394
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RESULT 11
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GENERAL INFORMATION:
 APPLICANT: Mutter, George
 APPLICANT: Baek, Jan
 TITLE OF INVENTION: Prognostic Classification of Breast Cancer
 FILE REFERENCE: B0801/7224(JRV)
 CURRENT APPLICATION NUMBER: US/09/917,254
 CURRENT FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: US 60/222,093
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 86
 LENGTH: 3110
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-09-917-254-86

Query Match 20.0%; Score 6; DB 4; Length 3110;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
 Db 389 NCERTCT 394

RESULT 14
 US-09-949-016-5937
 Sequence 5937, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 5937
 LENGTH: 3110
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-5937

Query Match 20.0%; Score 6; DB 4; Length 3110;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
 Db 389 NCERTCT 394

RESULT 15
 US-08-460-309-4
 Sequence 4, Application US/08460309
 Patent No. 5837496
 GENERAL INFORMATION:
 APPLICANT: Enyvall, Eva
 APPLICANT: Ielivo, Ilmo
 TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
 TITLE OF INVENTION: Fragments and Uses Thereof
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,309
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/125,077
 FILING DATE: 22-SEP-1993
 APPLICATION NUMBER: US PCT/US 94/10730
 FILING DATE: 21-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/472,319
 FILING DATE: 30-JAN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/919,951
 FILING DATE: 27-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9721
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-460-309-4

Query Match 20.0%; Score 6; DB 2; Length 3111;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
 Db 389 NCERTCT 394

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:33:36 ; Search time 33.4909 Seconds
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Title: US-09-977-406A-90

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	16	53.3	16	US-09-977-406A-10
5	16	53.3	17	US-09-977-406A-11
6	16	53.3	18	US-09-977-406A-12
7	16	53.3	19	US-09-977-406A-13
8	16	53.3	20	US-09-977-406A-14
9	16	53.3	21	US-09-977-406A-15
10	16	53.3	22	US-09-977-406A-16
11	16	53.3	23	US-09-977-406A-17
12	16	53.3	24	US-09-977-406A-18
13	16	53.3	25	US-09-977-406A-19

14	16	53.3	26	US-09-977-406A-20	Sequence 20, Appl
15	16	53.3	27	US-09-977-406A-21	Sequence 21, Appl
16	16	53.3	28	US-09-977-406A-22	Sequence 22, Appl
17	16	53.3	29	US-09-977-406A-23	Sequence 23, Appl
18	16	53.3	30	US-09-977-406A-24	Sequence 24, Appl
19	16	53.3	31	US-09-977-406A-25	Sequence 25, Appl
20	16	53.3	32	US-09-977-406A-26	Sequence 26, Appl
21	16	53.3	33	US-09-977-406A-27	Sequence 27, Appl
22	16	53.3	34	US-09-977-406A-28	Sequence 28, Appl
23	16	53.3	35	US-09-977-406A-29	Sequence 29, Appl
24	16	53.3	36	US-09-977-406A-30	Sequence 30, Appl
25	16	53.3	37	US-09-977-406A-31	Sequence 31, Appl
26	16	53.3	38	US-09-977-406A-32	Sequence 32, Appl
27	16	53.3	39	US-09-977-406A-33	Sequence 33, Appl
28	16	53.3	40	US-09-977-406A-34	Sequence 34, Appl
29	16	53.3	41	US-09-977-406A-35	Sequence 35, Appl
30	16	53.3	42	US-09-977-406A-36	Sequence 36, Appl
31	16	53.3	43	US-09-977-406A-37	Sequence 37, Appl
32	16	53.3	44	US-09-977-406A-38	Sequence 38, Appl
33	16	53.3	45	US-09-977-406A-39	Sequence 39, Appl
34	16	53.3	46	US-09-977-406A-40	Sequence 40, Appl
35	16	53.3	47	US-09-977-406A-41	Sequence 41, Appl
36	16	53.3	48	US-09-977-406A-42	Sequence 42, Appl
37	16	53.3	49	US-09-977-406A-43	Sequence 43, Appl
38	16	53.3	50	US-09-977-406A-44	Sequence 44, Appl
39	16	53.3	51	US-09-977-406A-45	Sequence 45, Appl
40	16	53.3	52	US-09-977-406A-46	Sequence 46, Appl
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42	16	53.3	54	US-09-977-406A-48	Sequence 48, Appl
43	16	53.3	55	US-09-977-406A-49	Sequence 49, Appl
44	16	53.3	56	US-09-977-406A-50	Sequence 50, Appl
45	16	53.3	57	US-09-977-406A-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-977-406A-90
; Sequence 90, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCTON PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-90

Query Match 100.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred.No. 1.3e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-977-406A-91
; Sequence 91, Application US/09977406A

Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-91

Query Match 100.0%; Score 30; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.9e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
Db 1 EMQDNCETCTCYETEMQDNCETCTCYET 30

RESULT 3
US-09-977-406A-92
; Sequence 92, Application US/09977406A
; Publication No. US20030170220A1

; GENERAL INFORMATION:
; APPLICANT: PROCON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-92

Query Match 100.0%; Score 30; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.4e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
Db 1 EMQDNCETCTCYETEMQDNCETCTCYET 30

RESULT 4
US-09-977-406A-10
; Sequence 10, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-10

Query Match 53.3%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETE 16
Db 1 EMQDNCETCTCYETE 16

RESULT 5
US-09-977-406A-11

; Sequence 11, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-11

Query Match 53.3%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETE 16
Db 1 EMQDNCETCTCYETE 16

RESULT 6
US-09-977-406A-12
; Sequence 12, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12

LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-12

Query Match 53.3%; Score 16; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
Db 1 EMQDNCETCTCYETE 16

RESULT 7
US-09-977-406A-13
Sequence 13, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-13

Query Match 53.3%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
Db 1 EMQDNCETCTCYETE 16

RESULT 8
US-09-977-406A-14
Sequence 14, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-14

Query Match 53.3%; Score 16; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
Db 1 EMQDNCETCTCYETE 16

RESULT 9
US-09-977-406A-15
Sequence 15, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-15

Query Match 53.3%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
Db 1 EMQDNCETCTCYETE 16

RESULT 10
US-09-977-406A-16
Sequence 16, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-16

Query Match 53.3%; Score 16; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
Db 1 EMQDNCETCTCYETE 16

RESULT 11
US-09-977-406A-17
; Sequence 17, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-17

Query Match 53.3%; Score 16; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 12
US-09-977-406A-18
; Sequence 18, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-18

Query Match 53.3%; Score 16; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 13
US-09-977-406A-19
; Sequence 19, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-19

Query Match 53.3%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 14
US-09-977-406A-20
; Sequence 20, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-20

Query Match 53.3%; Score 16; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 15
US-09-977-406A-21
; Sequence 21, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16

; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-19

Query Match 53.3%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 14
US-09-977-406A-20
; Sequence 20, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-20

Query Match 53.3%; Score 16; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 15
US-09-977-406A-21
; Sequence 21, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16

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; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-21

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Query Match      53.3%; Score 16; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EMQTDNCETCTCYETE 16
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Db      1 EMQTDNCETCTCYETE 16

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Job time : 33.4909 secs

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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:12:38 ; Search time 10.8 Seconds
(without alignments)
267.269 Million cell updates/sec

Title: US-09-977-406A-90

Sequence: 1 EMQDNCETCTCYETEMQDNCETCTCYET 30

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 79:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	53.3	114	2 A34567	beta-microseminopr
2	16	20.0	326	2 UC7094	nine-heme cytochro
3	6	20.0	601	2 B96744	unknown protein [i
4	6	20.0	895	2 T32374	hypothetical prote
5	6	20.0	1045	2 A29840	serine proteinase
6	5	16.7	38	2 JN0613	defensin 4K - scor
7	5	16.7	38	2 S27242	defensin - blue da
8	5	16.7	83	2 SS3116	methionine adenosy
9	5	16.7	91	2 SS2089	transcription fact
10	5	16.7	114	2 A54653	seminal plasma pro
11	5	16.7	119	1 S73864	hypothetical prote
12	5	16.7	127	2 S69429	conserved hypotet
13	5	16.7	130	2 G65019	hypothetical prote
14	5	16.7	155	2 F81108	toxin-activating p
15	5	16.7	167	2 C86241	protein T16B5.9 [i
16	5	16.7	210	2 AC2316	transposase alr408
17	5	16.7	226	2 C70962	hypothetical prote
18	5	16.7	246	2 A81679	conserved hypotet
19	5	16.7	256	2 T05554	hypothetical prote
20	5	16.7	281	2 A11064	probable outer mem
21	5	16.7	295	2 S76738	hypothetical prote
22	5	16.7	295	2 S76738	hypothetical prote
23	5	16.7	301	2 T26546	hypothetical prote
24	5	16.7	315	2 S66038	yac protein Bac
25	5	16.7	317	2 C83652	hypothetical prote
26	5	16.7	319	1 C70930	transcription fact
27	5	16.7	319	1 C70930	hypothetical prote
28	5	16.7	334	2 D82803	glyceraldehyde-3-p
29	5	16.7	339	2 T16273	hypothetical prote

30	5	16.7	340	1 B55973	transcription fact
31	5	16.7	347	2 AC0825	anaerobic sulfite
32	5	16.7	347	2 A38453	anaerobic sulfite
33	5	16.7	349	1 I50369	transcription fact
34	5	16.7	358	1 A55973	transcription fact
35	5	16.7	358	1 A55973	transcription fact
36	5	16.7	359	1 I51735	transcription fact
37	5	16.7	360	1 A55198	transcription fact
38	5	16.7	360	2 T06592	methionine adenosy
39	5	16.7	361	2 I50505	gene wnt8 protein
40	5	16.7	363	1 C55973	transcription fact
41	5	16.7	366	2 S66351	methionine adenosy
42	5	16.7	374	2 S41758	heat shock protein
43	5	16.7	374	2 C97058	molecular chaperon
44	5	16.7	385	2 C83817	coproporphyrinogen
45	5	16.7	390	2 S46540	methionine adenosy

ALIGNMENTS

RESULT 1
A34567
beta-microseminoprotein precursor - human
N:Alternate names: beta-inhibin, prostatic secretory protein, PSP-94; seminal plasma pro
C:Species: Homo sapiens (man)
C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text change 09-Jul-2004
C/Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682
R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein g
A:Reference number: A34567; MUID:90211299; PMID:2332265
A:Accession: A34567
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-114 <GRE>
A:Cross-references: UNIPROT:P08118; GB:M34376; NID:G514370; PID:AAA59871.1; PID:G514372
R:Mokey, M.; Nollet, S.; Fournier, S.; Benjanne, S.; Chappelaine, P.; Paradis, G.; Dube
DNA 6, 23-29, 1987
A:Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma p
A:Reference number: A26451; MUID:87161231; PMID:3829888
A:Accession: A26451
A:Molecule type: mRNA
A:Residues: 1-114 <MEI>
A:Cross-references: GB:M15885; NID:G338414; PID:AAA36635.1; PID:G338415
R:Akiyama, K.; Yoshitaka, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara, M
Biochim. Biophys. Acta 829, 288-294, 1985
A:Title: The amino acid sequence of human beta-microseminoprotein.
A:Reference number: A29777; MUID:85199974; PMID:3995056
A:Accession: A29777
A:Molecule type: protein
A:Residues: 21-58, 'PT', 61-113 <AKI>
R:Seidah, N.G.; Arbatli, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.
FEBS Lett. 175, 349-355, 1984
A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction o
A:Reference number: A30984; MUID:85004133; PMID:6434350
A:Accession: A30984
A:Molecule type: protein
A:Residues: 21-112, 'G', 114 <SEI>
R:Weiber, H.; Andersson, C.; Jurne, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
Am. J. Pathol. 137, 593-604, 1990
A:Title: Beta microseminoprotein is not a prostate-specific protein.
A:Reference number: A60673; MUID:90379237; PMID:2205099
A:Accession: A60673
A:Molecule type: protein
A:Residues: 21, 'X', 23-34 <MEI>
R:Nollet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16238
A:Molecule type: DNA

A:Residues: 1-114 <NOL>
 A:Cross-references: EMBL:X57928; NID:G35760; PIDN:CAA41002.1; PID:G825707
 A:Note: the authors translated the codon ACT for residue 54 as Trp
 R:Lin, A.Y.; Bradner, R.C.; Vessella, R.L.
 Cancer Lett. 74, 91-99, 1993
 A:Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.
 A:Reference number: 152682; MUID:94115955; PMID:7506990
 A:Accession: 152682
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-114 <RES>
 A:Cross-references: GB:S67815; NID:G460568; PIDN:AAB29732.1; PID:G460569
 A:Comment: This protein is a component of seminal plasma as well as secretory fluids from
 C:Genetics:
 A:Gene: GDB:MSMB
 A:Cross-references: GDB:128042; OMIM:157145
 A:Map position: 10q11.2-10q11.2
 A:Introns: 1/3; 37/1; 72/2
 C:Superfamily: seminal plasma protein
 C:Keywords: semen
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 53.3%; Score 16; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1,1e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWOTDNCERTCTCYETE 16
 |||||
 DB 51 EWOTDNCERTCTCYETE 66

RESULT 2

UC7094
 nine-heme cytochrome c - Desulfovibrio desulfuricans
 C:Species: Desulfovibrio desulfuricans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: J07094
 R:Saraiya, L.M.; da Costa, P.N.; Legall, J.
 Biochem. Biophys. Res. Commun. 262, 629-634, 1999
 A:Title: Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774 nine-heme c
 A:Reference number: J07094; MUID:99400423; PMID:10471375
 A:Accession: J07094
 A:Molecule type: DNA
 A:Residues: 1-326 <SAR>
 A:Cross-references: UNIPROT:Q9RNE6; GB:AF186393; NID:G5924394; PIDN:AAD56586.1; PID:G592
 A:Experimental source: ATCC 27774
 C:Genetics:
 A:Gene: 9HCC
 C:Keywords: electron transfer; heme; heme binding

Query Match 20.0%; Score 6; DB 2; Length 326;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 DNCERT 10
 |||||
 DB 75 DNCERT 80

RESULT 3

B96744
 unknown protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: B96744
 R:Theologis, A.; Ecker, J.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Aasen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11150712
 A:Accession: B96744
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-601 <STO>
 A:Cross-references: UNIPROT:Q9C7H2; GB:AE005173; NID:G11054407; PIDN:AAG27794.1; GSPDB:GN
 C:Genetics:
 A:Gene: F28P5.4
 A:Map position: 1

Query Match 20.0%; Score 6; DB 2; Length 601;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CERTCTC 12
 |||||
 DB 514 CERTCTC 519

RESULT 4

T32374
 hypothetical protein K10F12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
 C:Accession: T32374
 R:Wohlmann, P.; Beck, C.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of C. elegans cosmid K10F12.
 A:Reference number: Z21157
 A:Accession: T32374
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-895 <WOH>
 A:Cross-references: EMBL:AF025462; PIDN:AAB71005.1; GSPDB:GN00021; CESP:K10F12.3
 A:Experimental source: strain Bristol N2; clone K10F12
 C:Genetics:
 A:Gene: CESP:K10F12.3

A:Map position: 3
 A:Introns: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 624
 C:Superfamily: Yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phospho
 sphodiesterase domain Y homolog
 F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 20.0%; Score 6; DB 2; Length 895;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TDNCERT 9
 |||||
 DB 288 TDNCERT 293

RESULT 5

A29840
 serine proteinase (EC 3.4.21.-) precursor - Serratia marcescens (strain IFO-3046)
 C:Species: Serratia marcescens
 C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C:Accession: A29840
 R:Yanagida, N.; Uozumi, T.; Beppu, T.
 J. Bacteriol. 166, 937-944, 1986
 A:Title: Specific excretion of Serratia marcescens protease through the outer membrane of
 A:Reference number: A29840; MUID:86223815; PMID:3011754
 A:Accession: A29840
 A:Molecule type: DNA
 A:Residues: 1-1045 <YAN>
 A:Cross-references: UNIPROT:P09489; GB:M13469; NID:G152857; PIDN:AAA26572.1; PID:G152858
 C:Superfamily: autotransporter subtilisin-like protease precursor; subtilisin homology
 C:Keywords: hydrolase; serine proteinase
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-408/Product: serine proteinase #status predicted <MAT>

F:67-355/Domain: subtilisin homology <SBT>
F:409-1045/Domain: carboxyl-terminal propeptide #status predicted <Pro>
F:76,112,341/Active site: Asp, His, Ser #status predicted

Query Match 20.0%; Score 6; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TEMOTD 20
Db 953 TEMOTD 958

RESULT 6

JN0613
defensin 4K - scorpion (Leiurus quinquestriatus)
N/Alternate names: antibacterial 4K peptide
C/Species: Leiurus quinquestriatus hebraeus
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0613

R/Cociancich, S.; Goyffon, M.; Bontems, F.; Bulet, P.; Bouet, F.; Menez, A.; Hoffmann, J.
Biochem. Biophys. Res. Commun. 194, 17-22, 1993
A/Title: Purification and characterization of a scorpion defensin, a 4kDa antibacterial
A/Reference number: JN0613; PMID:93326112; PMID:8333834
A/Accession: JN0613

A/Molecule type: protein
A/Residues: 1-38 <COC>
A/Cross-references: UNIPROT:P41965
A/Note: this protein is similar to scorpion toxins and insect defensins

Query Match 16.7%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TCTCY 13
Db 32 TCTCY 36

RESULT 7

S27242
defensin - blue darter
C/Species: Aeschna cyanea (blue darter)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S27242

R/Bulet, P.; Cociancich, S.; Reuland, M.; Sauber, F.; Bischoff, R.; Hegy, G.; van Dorssse
Eur. J. Biochem. 209, 977-984, 1992
A/Title: A novel insect defensin mediates the inducible antibacterial activity in larvae
A/Reference number: S27242; PMID:93049356; PMID:1425705
A/Accession: S27242

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-38 <BUL>
A/Cross-references: UNIPROT:P80154

Query Match 16.7%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TCTCY 13
Db 33 TCTCY 37

RESULT 8

SS3116
methionine adenosyltransferase (EC 2.5.1.6) - chickpea (fragment)
N/Alternate names: S-adenosylmethionine synthetase
C/Species: Cicer arietinum (chickpea, garbanzo)
C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: SS3116

R/Cervantes, E.
submitted to the EMBL Data Library, March 1995

A/Reference number: SS3116
A/Accession: SS3116
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-83 <CER>

A/Cross-references: UNIPROT:Q39465; EMBL:X85252; NID:g1808591; PIDN:CAA59508.1; PID:g732
C/Superfamily: methionine adenosyltransferase
C/Keywords: S-adenosylmethionine; transferase

Query Match 16.7%; Score 5; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CETCT 11
Db 43 CETCT 47

RESULT 9

SS2089
transcription factor isl-2a (clone S3) - chinook salmon
N/Alternate names: insulin enhancer-binding protein isl-2a; islet-2a protein
C/Species: Oncorhynchus tshawytscha (chinook salmon)
C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C/Accession: SS2089

R/Gong, Z.; Hew, C.L.
Biochim. Biophys. Acta 1260, 349-354, 1995
A/Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus tshawytscha)
A/Reference number: SS2089; PMID:95178560; PMID:7873614
A/Accession: SS2089

A/Molecule type: mRNA
A/Residues: 1-91 <GON>
A/Cross-references: EMBL:X64882
A/Experimental source: clone S3
C/Genetics:

A/Gene: isl-2a
C/Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat h
C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati
F:3-56/Domain: LIM metal-binding repeat homology <LIM>

Query Match 16.7%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 ETCCT 12
Db 40 ETCCT 44

RESULT 10

AS4663
seminal plasma protein PSP-94 precursor - rhesus macaque
N/Alternate names: prostatic secretory protein PSP94
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C/Accession: S16237; AS4663

R/Nolet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A/Reference number: S16237; PMID:91274357; PMID:2054385
A/Accession: S16237

A/Molecule type: DNA
A/Residues: 1-114 <NO2>
A/Cross-references: UNIPROT:P25142; EMBL:X57932; NID:g38094; PIDN:CAA41003.1; PID:g82915;
A/Note: the authors translated the codon ACT for residue 54 as TTP
R/Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.
Genomics 9, 775-777, 1991

A/Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence bet
A/Reference number: AS4663; PMID:91244325; PMID:2037304
A/Accession: AS4663
A/Molecule type: mRNA
A/Residues: 1-114 <NO2>
A/Cross-references: GB:M92161; NID:g342280; PIDN:AAA36903.1; PID:g342281

C/Genetics:
A/Intons: 1/3; 37/1; 72/2
C/Superfamily: seminal plasma protein
P.1-20/Domain: signal sequence #status predicted <SIG>

Query Match 16.7%; Score 5; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

S73864
hypothetical protein H10_orf119 - Mycoplasma pneumoniae (strain ATCC 29342)

C/Species: Mycoplasma pneumoniae
A/Variety: ATCC 29342
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S73864
R/Himmelreich, R.; Hilbert, H.; Plogens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A/Reference number: S73327; PMID:97105885; PMID:8948633
A/Accession: S73864
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1119 <HIM>
A/Cross-references: UNIPROT:P75480; EMBL:AE000052; GB:U00089; NID:G1674223; PIDN:AAB9618
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C/Genetics:
A/Genetic code: SGC3
C/Superfamily: holo-ACP synthase

Query Match 16.7%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTDNC 7
DB 21 QTDNC 25

RESULT 12

B69429
conserved hypothetical protein AF1438 - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: B69429
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glock, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A/Authors: Ueberbach, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A/Reference number: A69250; PMID:98049343; PMID:9389475
A/Accession: B69429
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-127 <MLE>
A/Cross-references: UNIPROT:Q28834; GB:AE001004; GB:AE000782; NID:G2689327; PIDN:AAB9881

Query Match 16.7%; Score 5; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CYETE 16
DB 16 CYETE 20

RESULT 13

G65019
hypothetical protein b2448 - Escherichia coli (strain K-12)

C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: G65019
R/Plattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Sho, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; PMID:97426617; PMID:9278503
A/Accession: G65019
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-130 <BLAT>
A/Cross-references: UNIPROT:P76548; GB:AE000332; GB:U00096; NID:G1788789; PIDN:AAC75501.1
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: Escherichia coli hypothetical protein b2448

Query Match 16.7%; Score 5; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8
DB 43 TDNCE 47

RESULT 14

F81108
toxin-activating protein, probable NMB1210 [imported] - Neisseria meningitidis (strain MC

C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C/Accession: F81108
R/Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scariato, V.; Masiogni, V.; Piazza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; PMID:20175755; PMID:10710307
A/Accession: F81108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-155 <TEP>
A/Cross-references: UNIPROT:Q9U7B0; GB:AE002469; GB:AE002098; NID:G7226446; PIDN:AAF1597
A/Experimental source: serogroup B, strain MC58
C/Genetics:
A/Genetic code: NMB1210
C/Superfamily: hemolysin C

Query Match 16.7%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ETEWQ 18
DB 80 ETEWQ 84

RESULT 15

C66241
protein T16B5.9 [imported] - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C66241
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luvos, J.S.; Maltli, R.; Marzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-167 <STO>
A:Cross-references: UNIPROT:Q9SACS; GB:AE005172; NID:94874271; PIDN:ADJ1336.1; GSPDB:GN
C:Genetics:
A:Gene: T16B5.9
A:Map position: 1

Query Match 16.7%; Score 5; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TCYET 15
|||
|||
Db 91 TCYET 95

Search completed: May 4, 2005, 14:34:57
Job time : 11.8 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:04:27 ; Search time 51.4909 Seconds
(without alignments)
298.351 Million cell updates/sec

Title: US-09-977-406A-90
Perfect score: 30
Sequence: 1 EMQTDNCETCTCYETEMQTDNCETCTCYET 30

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	53.3	114	1 MSMB_HUMAN	P08118 homo sapien
2	7	23.3	114	7 MSMB_PAPAN	O28767 papio anubi
3	6	20.0	196	2 Q9D8T1	O28871 mus musculu
4	6	20.0	215	2 Q7V5F4	Q7V5F4 prochloroc
5	6	20.0	326	1 CYC9_DESDE	Q9N68 desulfovibr
6	6	20.0	459	1 MURD_LACPL	O88W80 lactobacill
7	6	20.0	601	2 Q9C7H2	O9C7H2 arabidopsis
8	6	20.0	1045	1 PRTS_SERMA	P09489 serraria ma
9	6	20.0	1068	2 O81A76	O81A76 caenorhabdi
10	6	20.0	1075	2 O81A75	O81A75 caenorhabdi
11	6	20.0	1615	2 Q7QZU9	Q7QZU9 giardia lam
12	6	20.0	1870	2 Q7OH34	Q7OH34 fowlpox vir
13	6	20.0	1870	2 Q9J5A0	Q9J5A0 fowlpox vir
14	6	20.0	3110	1 LMA2_HUMAN	P24043 homo sapien
15	5	16.7	37	1 DEF4_ANDAU	P66668 androctonus
16	5	16.7	38	1 DEF4_LEIOH	P80154 leiturus qui
17	5	16.7	38	1 DEF1_AESCY	P80154 aescyna cya
18	5	16.7	51	2 Q7Y3N1	Q7Y3N1 enterobacte
19	5	16.7	54	2 Q24985	Q24985 giardia lam
20	5	16.7	58	2 O8FCX2	O8FCX2 escherichia
21	5	16.7	70	2 O8R5C3	O8R5C3 mus musculu
22	5	16.7	74	1 DEF1_DERVA	O6753 dermaceutor
23	5	16.7	74	2 O86LE4	O86LE4 boophilus m
24	5	16.7	75	2 O8JX66	O8JX66 sen virus.
25	5	16.7	75	2 O8JX67	O8JX67 sen virus.
26	5	16.7	77	2 O8C1L6	O8C1L6 mus musculu
27	5	16.7	81	2 O6VY76	O6VY76 bacterioph
28	5	16.7	83	2 Q39465	Q39465 cicet ariet
29	5	16.7	105	2 Q8B077	Q8B077 mus musculu
30	5	16.7	110	2 Q42169	Q42169 arabidopsis
31	5	16.7	111	2 Q9JH97	Q9JH97 unclassified

32	5	16.7	112	2 Q854B7	Q854B7 mycobacteri
33	5	16.7	113	2 Q22079	Q22079 nicotiana t
34	5	16.7	114	2 MSMB_MACMU	P25142 macaca mula
35	5	16.7	114	2 Q8L2M3	Q8L2M3 helicobacte
36	5	16.7	115	2 Q7KTX0	Q7KTX0 drosophila
37	5	16.7	117	2 Q8A7Y2	Q8A7Y2 bacteroides
38	5	16.7	119	1 ACPS_MYCPN	P75480 mycoplasma
39	5	16.7	121	2 Q7ZGB3	Q7ZGB3 human immu
40	5	16.7	127	2 Q28834	Q28834 archaeoglob
41	5	16.7	127	2 Q6IKD4	Q6IKD4 drosophila
42	5	16.7	130	1 YFPQ_ECOLI	P76548 escherichia
43	5	16.7	131	2 Q8CPD4	Q8CPD4 mus musculu
44	5	16.7	132	2 Q97442	Q97442 giardia lam
45	5	16.7	133	2 Q6PRE3	Q6PRE3 helicobacte

ALIGNMENTS

RESULT 1	MSMB_HUMAN	STANDARD	PRT	114 AA.
AC	P08118; P11999; Q13125; Q9UC59;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	05-JUN-2004 (Rel. 44, Last annotation update)			
DE	Beta-microglobulin precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PNA44).			
GN	Name=MSMB; Synonyms=PRSP;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
NCBI_TaxID=9606;				
LN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87161231; PubMed=3829888;			
RA	Molloy M., Nole S., Fournier S., Benjannet S., Chapelaine P., Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidah N.G., Chretien M.,			
RA	"Molecular cloning and sequence of the cDNA for a 94-amino-acid			
RT	seminal plasma protein secreted by the human prostate.";			
RL	DNA 6:23-29(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91274357; PubMed=2054385; DOI=10.1016/0167-4781(91)90016-F;			
RA	Nolet S., Molloy M., Chretien M.,			
RT	"Prostatic secretory protein PSP94: gene organization and promoter			
RT	sequence in rhesus monkey and human.";			
RL	Biochim. Biophys. Acta 1069:247-249(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90211299; PubMed=2322265;			
RA	Green C.B., Liu W.Y., Kwok S.C.M.,			
RT	"Cloning and nucleotide sequence analysis of the human beta-			
RT	microseminoprotein gene.";			
RL	Biochem. Biophys. Res. Commun. 167:1184-1190(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90073664; PubMed=2590204;			
RA	Uvshbeck M., Lindstrom C., Weiber H., Abrahamsson P.-A., Lilja H., Lundwall A.,			
RT	"Molecular cloning of a small prostate protein, known as beta-			
RT	microseminoprotein, PSP94 or beta-inhibin, and demonstration of			
RL	transcripts in non-genital tissues.";			
RL	Biochem. Biophys. Res. Commun. 164:1310-1315(1989).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=94115955; PubMed=7506990; DOI=10.1016/0304-3835(93)90049-F;			
RA	Liu A.Y., Bradner R.C., Vessella R.L.,			
RT	"Decreased expression of prostatic secretory protein PSP94 in prostate			
RT	cancer.";			

FT VARSPIC 78 114 Missing (in isoform PSP57).
/Frid=VSP_003276.
FT
Query Match 53.3%; Score 16; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EMOTNCCTCTCYETE 16
| | | | | | | | | | | | | | | | | | | | | |
Db 51 EMOTNCCTCTCYETE 66

RESULT 2
MSMB PAPAN STANDARD; PRT; 114 AA.
AC Q28767;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (ESP-94).
GN Name=MSMB; Synonym=PSPP94;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9555;
RN (1)
RC SEQUENCE FROM N.A.
RP TISSUE=Prostate;
RX MEDLINE=97316893; PubMed=9174167;
RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., McKay M., Zhong R.,
RA Chin J.L.;
RT "Molecular cloning and gene expression analysis of PSP94 (prostate secretory protein of 94 amino acids) in primates.";
RL DNA Cell Biol. 16:627-638(1997).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC
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CC
CC EMBL; U49786; AAB63726.1; -
DR InterPro: IPR008735; PSP94.
DR Pfam: PF05825; PSP94; 1.
KW Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 114 Beta-microseminoprotein.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.
FT DISULFID 60 69 Or C-60 with C-70 (By similarity).
FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT DISULFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98BD CRC64;
Query Match 23.3%; Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 WQDNCNCE 8
| | | | | | | | | | | | | | | | | | | | | |
Db 52 WQDNCNCE 58

RESULT 3
Q9DBY1 PRELIMINARY; PRT; 196 AA.
AC Q9DBY1;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:1810020B01 product:hypothetical protein, full insert sequence (RIKEN cDNA 1810020B01).
DE Name=1810020B01Rik;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN (2)
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN (3)
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The PANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team; analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN (4)
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN (5)
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishire T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara S., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN (6)
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito R., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki H., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Segabe Y., Suzuki D., Tagami M., Tagami A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN (7)
RC SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Stenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguailano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKean P.U., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK007559; BAB5107.1; -
 DR EMBL; BC023171; AAH23171.1; -
 DR MCD; MG11913521; 1810020E01R1K.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR009801; DUF1370.
 DR Pfam; PF07114; DUF1370; 1.
 KM Hypothetical protein.
 SO SEQUENCE 196 AA; 21539 MW; 994P5E2251C5FEB CRC64;

Query Match 20.0%; Score 6; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
 DB 98 NCETCT 103

RESULT 4
 07V5F4 PRELIMINARY; PRT; 215 AA.
 AC 07V5F4;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Bacterial regulatory proteins, AsnC family.
 GN Ordered locus names=PM1607;
 OS Prochlorococcus marinus (strain MIT 9313).
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococaceae;
 OC Prochlorococcus.
 NCBI_TaxID=74547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22525686; PubMed=12917642; DOI=10.1038/nature01947;
 RA Rospal G., Larimer F.W., Lamerdin J.E., Malifati S., Chain P.,
 RA Ahlberg N.A., Ariellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
 RT niche differentiation.";
 RT Nature 424:1042-1047(2003).
 RL EMBL; BX572099; CAE21782.1; -
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 KW Complete proteome.
 SO SEQUENCE 215 AA; 24165 MW; E663AA68A216D0C5 CRC64;

Query Match 20.0%; Score 6; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YETEMQ 18
 DB 142 YETEMQ 147

RESULT 5
 CYC9 DESDE STANDARD; PRT; 326 AA.
 ID CYC9 DESDE
 AC 09RN68;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Nine-heme cytochrome c precursor (9Hcc).
 OS Desulfovibrio desulfuricans.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 NCBI_TaxID=876;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99400423; PubMed=10471375; DOI=10.1006/bbrc.1999.1238;
 RA Saraiya L.M., da Costa P.N., Legall J.;
 RT "Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774
 RT nine-heme cytochrome c.";
 RT Biochem. Biophys. Res. Commun. 262:629-634(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=20022508; PubMed=10555582;
 RA Matias P.M., Saraiya L.M., Soares C.M., Coelho A.V., Legall J.,
 RA Carrondo M.A.;
 RT "Nine-haem cytochrome c from Desulfovibrio desulfuricans ATCC 27774:
 RT primary sequence determination, crystallographic refinement at 1.8 Å
 RT and modelling studies of its interaction with the tetrahaem cytochrome
 RT c3.";
 RT J. Biol. Inorg. Chem. 4:478-494(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99148120; PubMed=10366280; DOI=10.1016/S0969-2126(99)80019-7;
 RA Matias P.M., Coelho R., Pereira I.A.C., Coelho A.V., Thompson A.W.,
 RA Steker L., Legall J., Carrondo M.A.;
 RT "The primary and three-dimensional structures of a nine-haem
 RT cytochrome c from Desulfovibrio desulfuricans ATCC 27774 reveal a new
 RT member of the Hmc family.";
 RL Structure 7:119-130(1999).
 CC -1- FUNCTION: May form part of a transmembrane redox complex through
 CC which electrons are transferred to the cytoplasm for reduction of
 CC sulfate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- DOMAIN: Arranged into two tetraheme clusters and the extra heme 4
 CC is located asymmetrically between the two regions.
 CC -1- PTM: Binds 9 heme groups per subunit.
 CC -1- SIMILARITY: Contains 9' cytochrome c domains.
 CC -----
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 CC -----
 DR EMBL; AF186393; AAD56586.1; -
 DR PIR; JC7094; JC7094.
 DR PDB; 19HC; X-ray; A/B=31-322.
 DR PDB; 10FW; X-ray; A/B=31-326.

DR PDB; 1OFY; X-ray; A/B=31-326.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR002322; Cyt CIII.
 DR InterPro; IPR011031; Multiheme_cyt.
 DR Pfam; PF02085; Cytochrom_cIII; 1.
 DR PRINTS; PR00609; CYTOCHROME_C3.
 DR PROSITE; PS51008; MULTIHEME_CYT_C; 1.
 DR 3D-structure; Electron transport; Heme; Periplasmic; Repeat; Signal.
 KM SIGNAL 1 30
 FT CHAIN 1 326 Nine-heme cytochrome C.
 FT METAL 67 67 Iron (heme 1 axial ligand).
 FT METAL 70 70 Iron (heme 3 axial ligand).
 FT BINDING 77 77 Heme 1 (covalent).
 FT BINDING 80 80 Heme 1 (covalent).
 FT METAL 81 81 Iron (heme 1 axial ligand).
 FT METAL 82 82 Iron (heme 2 axial ligand).
 FT BINDING 89 89 Heme 2 (covalent).
 FT BINDING 92 92 Heme 2 (covalent).
 FT METAL 93 93 Iron (heme 2 axial ligand).
 FT METAL 111 111 Iron (heme 5 axial ligand).
 FT BINDING 127 127 Heme 3 (covalent).
 FT BINDING 130 130 Heme 3 (covalent).
 FT METAL 131 131 Iron (heme 3 axial ligand).
 FT BINDING 141 141 Heme 4 (covalent).
 FT BINDING 144 144 Heme 4 (covalent).
 FT METAL 145 145 Iron (heme 4 axial ligand).
 FT BINDING 157 157 Heme 5 (covalent).
 FT BINDING 160 160 Heme 5 (covalent).
 FT METAL 161 161 Iron (heme 5 axial ligand).
 FT METAL 227 227 Iron (heme 6 axial ligand).
 FT METAL 230 230 Iron (heme 8 axial ligand).
 FT METAL 248 248 Iron (heme 4 axial ligand).
 FT BINDING 255 255 Heme 6 (covalent).
 FT BINDING 258 258 Heme 6 (covalent).
 FT METAL 259 259 Iron (heme 6 axial ligand).
 FT METAL 260 260 Iron (heme 7 axial ligand).
 FT BINDING 271 271 Heme 7 (covalent).
 FT BINDING 274 274 Heme 7 (covalent).
 FT METAL 275 275 Iron (heme 7 axial ligand).
 FT METAL 294 294 Iron (heme 9 axial ligand).
 FT BINDING 297 297 Heme 8 (covalent).
 FT BINDING 300 300 Heme 8 (covalent).
 FT METAL 301 301 Iron (heme 8 axial ligand).
 FT BINDING 314 314 Heme 9 (covalent).
 FT BINDING 317 317 Heme 9 (covalent).
 FT METAL 318 318 Iron (heme 9 axial ligand).
 FT STRAND 43 46
 FT TURN 55 56
 FT STRAND 63 66
 FT HELIX 67 73
 FT HELIX 77 80
 FT TURN 82 83
 FT TURN 89 91
 FT HELIX 92 92
 FT TURN 99 101
 FT HELIX 102 103
 FT HELIX 106 111
 FT HELIX 127 137
 FT HELIX 139 142
 FT TURN 143 143
 FT HELIX 144 147
 FT STRAND 154 160
 FT STRAND 161 161
 FT TURN 165 166
 FT HELIX 169 177
 FT TURN 178 178
 FT HELIX 182 195
 FT STRAND 204 206
 FT STRAND 211 213
 FT TURN 215 216
 FT STRAND 220 220
 FT STRAND 223 225
 FT HELIX 227 236

FT TURN 237 240
 FT HELIX 242 247
 FT TURN 251 252
 FT HELIX 253 257
 FT TURN 258 258
 FT HELIX 271 274
 FT TURN 281 282
 FT TURN 284 285
 FT HELIX 289 303
 FT TURN 304 305
 FT STRAND 311 312
 FT STRAND 320 320
 SQ SEQUENCE 326 AA; 2ED7025ADDF250E3 CRC64;
 Query Match 20.0%; Score 6; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 DNCETC 10
 Db 75 DNCETC 80
 RESULT 6
 MURD_LACPL STANDARD; PRT; 459 AA.
 AC O8BV80;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid adding enzyme).
 DE Name=murD; OrderedLocNames=lp_2197;
 GN Lactobacillus plantarum.
 OS Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxId=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; Pubmed=12566566; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M., Fiers W.W.E.J., Strekema W., Klein Lankhorst R.M., Bron P.A., Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B., De Vos W.M., Siezen R.J.;
 RA "Complete genome sequence of Lactobacillus plantarum WCFS1.";
 RA Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 RL
 CC -!- FUNCTION: Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (DHA) (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
 CC -!- PATHWAY: Peptidoglycan biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the murCDF family.
 CC
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 CC
 CC EMBL; AL935258; CAD64544.1; -.
 DR HSSP; P14900; 20AG.
 DR HAMAP; MF_00639; -; 1.
 DR InterPro; IPR004101; Mur_ligase_C.
 DR InterPro; IPR000713; Mur_ligase_N.
 DR InterPro; IPR005762; MurD.

DR Pfam; PF01225; Mur_Ligase; 1.
 DR Pfam; PF02875; Mur_Ligase_C; 1.
 KW ATP-binding; Cell Division; Cell wall; Complete proteome; Ligase;
 KW Peptidoglycan synthesis.
 SQ SEQUENCE 459 AA; 50137 MW; 083AB3E45C59DC9 CRC64;
 NP_BIND 119 125 ATP (Potential).
 Query Match 20.0%; Score 6; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCET 9
 DB 403 TDNCET 408

RESULT 7
 Q9C7H2 PRELIMINARY; PRT; 601 AA.
 AC Q9C7H2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein F28P5.4 (A01972090/F28P5_4).
 GN Name=F28P5.4;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maletti R., Renning C.M., Koo H., Fujii C.Y., Uterback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bowser L., Carrinci P., Chung M.K., Goldenrich A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carrinci P.,
 RA Chan M.W., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onda C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC069273; AAG51137.1; -
 DR EMBL; AF367274; AAK56263.1; -
 DR EMBL; BT002712; AAO11628.1; -
 DR PIR; B96744; B96744.
 DR GO; GO:0003824; F-catalytic activity; IEA.
 DR GO; GO:0005506; Filion ion binding; IEA.
 DR InterPro; IPR006638; E1p3/MiAB/NiIB.
 DR InterPro; IPR006466; MiAB like B.
 DR InterPro; IPR007197; Radical_SAM.
 DR InterPro; IPR002782; TRAM.
 DR InterPro; IPR005839; UPF0004.
 DR Pfam; PF04055; Radical_SAM; 1.
 DR Pfam; PF01938; TRAM; 1.
 DR Pfam; PF00919; UPF0004; 1.
 DR SMART; SM00729; E1p3; 1.
 DR TIGRFAMs; TIGR01578; MiAB-like-B; 1.
 DR TIGRFAMs; TIGR00089; UPF0004; 1.

DR PROSITE; PS0026; TRAM; 1.
 DR PROSITE; PS01278; UPF0004; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 601 AA; 65496 MW; AAC137F7EC3DA3D CRC64;
 NP_BIND 119 125 ATP (Potential).
 Query Match 20.0%; Score 6; DB 2; Length 601;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CETCTC 12
 DB 514 CETCTC 519

RESULT 8
 PRTS_SERMA
 ID PRTS_SERMA STANDARD; PRT; 1045 AA.
 AC P09489;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Extracellular serine protease precursor (EC 3.4.21.-).
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 NC NCB1_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-35 AND 407-408.
 RC STRAIN=IFO 3046;
 RX MEDLINE=86223815; PubMed=3011754;
 RA Yanagida N., Uozumi T., Beppu T.;
 RT "Specific excretion of Serratia marcescens protease through the outer
 RT membrane of Escherichia coli.";
 RL J. Bacteriol. 166:937-944(1986).
 RN [2]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=92348352; PubMed=1639760;
 RA Shikata S., Shimada K., Kataoka H., Hornouchi S., Beppu T.;
 RT "Detection of large COOH-terminal domains processed from the precursor
 RT of Serratia marcescens serine protease in the outer membrane of
 RL Escherichia coli.";
 RL J. Biochem. 111:627-632(1992).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the peptidase S8 family.
 CC
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 CC
 CC EMBL; M13469; AAA26572.1; -
 DR PIR; A29840; A29840.
 DR HSP; Q99405; IMPT.
 DR MEROPS; S08.094; -
 DR InterPro; IPR005546; Auto_transptbeta.
 DR InterPro; IPR006315; Auto_transporter.
 DR InterPro; IPR000209; Pept_S8_S53.
 DR InterPro; IPR011655; Pept_S8A_auftrans.
 DR Pfam; PF03797; Auto_transporter; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PIRSF; PIRSF00164; Autoc_t_spt-like; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR TIGRFAMs; TIGR01414; autocrans_bar1; 1.
 DR PROSITE; PS00136; SUBTILASE ASP; FALSE_NEG.
 DR PROSITE; PS00137; SUBTILASE HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Direct protein sequencing; Hydrolase; Serine protease; Signal;
 KW Zymogen.
 FT SIGNAL 1 27
 FT CHAIN 28 645 Extracellular serine protease.

FT	PROPER	646	1045	
FT	ACT_SITE	76	76	Charge relay system (By similarity).
FT	ACT_SITE	112	112	Charge relay system (By similarity).
FT	ACT_SITE	341	341	Charge relay system (By similarity).
SO	SEQUENCE	1045 AA;	112345 MW;	4924EA50E4FF179C CRC64;
Qy	15 TEMQTD	20		
Db	953 TEMQTD	958		
RESULT 9				
Q81A76				
Q81A76	PRELIMINARY;		PRT;	1068 AA.
AC	Q81A76;			
DT	01-MAR-2003 (TREMBLrel. 23, Created)			
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Phospholipase C like protein 1, isoform b.			
GN	Name=pl1-1; ORFNames=K10F12.3;			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Pelodertinae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
OX	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RX	MEDLINE=99063613; PubMed=9851916;			
RG	Wormbase Consortium;			
RT	"Genome sequence of the nematode C. elegans: a platform for			
RT	investigating biology. The C. elegans Sequencing Consortium. "			
RL	Science 282:2012-2018 (1998).			
RN	(2)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Wohlmann P., Beck C.;			
RT	"The sequence of C. elegans cosmid K10F12."			
RL	Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.			
RN	(3)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Waterston R.;			
RL	Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.			
RN	(4)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Wilson R.;			
RL	Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.			
RN	(5)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Wilson R.;			
RL	Submitted (DEC-2003) to the EMBL/Genbank/DBJ databases.			
RN	(6)			
RP	STRAIN=Bristol N2;			
RC	Wormbase Consortium;			
RL	Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.			
CC	-1- SIMILARITY: Contains 1 C2 domain.			
DR	EMBL; AF025462; AAN72423.1; -.			
DR	HSSP; P10688; IDH.			
DR	Wormbase; WBGene00004045; pl1-1.			
DR	WormPeP; K10F12.3b; CE31037.			
DR	GO; GO:0004435; F:phospholipase C activity; IEA.			
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.			
DR	GO; GO:0006629; P:lipid metabolism; IEA.			
DR	InterPro; IPR000008; C2.			
DR	InterPro; IPR008973; C2_CALB.			
DR	InterPro; IPR001849; PH.			

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DR InterPro: IPR0011036; PH related.
DR InterPro: IPR001192; PI_PLC.
DR InterPro: IPR000909; PI_PLC_X.
DR InterPro: IPR001711; PI_PLC_Y.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00388; PI-PLC-X; 1.
DR Pfam: PF00387; PI-PLC-Y; 1.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00390; PHPHILIPASEC.
DR ProDom: PD001202; PI_PLC_Y; 1.
DR SMART: SM00239; C2; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00148; PLCXc; 1.
DR SMART: SM00149; PLCYC; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS50007; PIPLC_X_DOMAIN; 1.
DR PROSITE: PS50008; PIPLC_Y_DOMAIN; 1.
SQ SEQUENCE 1068 AA; 120042 MW; 9BF7CFCFFD7EC221 CRG64;

Query Match      20.0%; Score 6; DB 2; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCET 9
Db 310 TDNCET 315

RESULT 10
O81A75 PRELIMINARY; PRT: 1075 AA.
ID O81A75;
AC O81A75;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform a.
GN Name=pl1-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RL investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wohldmann P., Beck C.;
RT "The sequence of C. elegans cosmid K10F12.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

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RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 C2 domain.
DR EMBL: AF025462; AA072422.1; -.
DR HSSP: P10688; IDUH.
DR WormBase; WBGene00004045; p11-1.
DR WormPep; K10F12.3a; CB31036.
DR GO: GO:0004435; F:phosphoinositide phospholipase C activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CalB.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH related.
DR InterPro; IPR011192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_X.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PPHILIPASEC.
DR ProDom; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00148; PLCXC; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2 DOMAIN 2; 1.
DR PROSITE; PS50007; PIPLC_X DOMAIN; 1.
DR PROSITE; PS50008; PIPLC_Y DOMAIN; 1.
DR SEQUENCE 1075 AA; 12111 MW; 6102111ABF78AFP4 CRC64;
SQ
Query Match 20.0%; Score 6; DB 2; Length 1075;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TNCCT 9
DB 317 TNCCT 322
RESULT 11
Q7QZU9 PRELIMINARY; PRT; 1615 AA.
ID Q7QZU9
AC Q7QZU9; TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE GLP_609_15416_20263.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.
ON NCBI_TaxID=184922;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RT Olsen G.J., Sogin M.L.;
RL "Direct sequence of the Giardia lamblia genome.";
CC Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; AACB01000040; BAA40566.1; -.
DR HSSP; P35555; 1EMN.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR005127; Giardia_VSP.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR002049; laminin_EGF.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00053; laminin_EGF; 1.
DR Pfam; PF03302; VSP; 1.

DR PROSITE; PS00022; EGF_1; 4.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 4.
DR SEQUENCE 1615 AA; 169595 MW; B88E3D60D1B4F27 CRC64;
SQ
Query Match 20.0%; Score 6; DB 2; Length 1615;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 DNCCTC 10
DB 1261 DNCCTC 1266
RESULT 12
Q7OH34 PRELIMINARY; PRT; 1870 AA.
ID Q7OH34
AC Q7OH34;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE VAVV Bangladesh B22R orthologue.
GN Name=fp9.122;
OS Fowlpox virus (isolate HP-438[Munich]).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
ON Avipoxvirus.
ON NCBI_TaxID=10263;
RN [1]
RP SEQUENCE FROM N.A.
RA Skinner M.A., Laidlaw S.M.;
RT "Comparison of the genome sequence of FP9, an attenuated, tissue
culture-adapted European fowlpox virus, with those of virulent
American and European viruses.";
RL J. Gen. Virol. 85:305-322(2004).
DR EMBL; AJ581527; CAES2663.1; -.
DR InterPro; IPR007490; Poxvirus_B22R.
DR Pfam; PF04395; Poxvirus_B22R; 1.
DR SEQUENCE 1870 AA; 211756 MW; 2423D319743D3F2F CRC64;
SQ
Query Match 20.0%; Score 6; DB 2; Length 1870;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 NCCTCT 11
DB 241 NCCTCT 246
RESULT 13
Q9J5A0 PRELIMINARY; PRT; 1870 AA.
ID Q9J5A0
AC Q9J5A0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE ORF_FPV122 variola B22R gene family protein.
GN Name=FPV122;
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
ON Avipoxvirus.
ON NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RX DOI=10.1128/JVI.74.8.3815-3831.2000;
RA Alfonso C.U., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
DR EMBL; AF198100; AAF44466.1; -.
DR InterPro; IPR007490; Poxvirus_B22R.
DR Pfam; PF04395; Poxvirus_B22R; 1.
DR SEQUENCE 1870 AA; 211756 MW; 2423D319743D3F2F CRC64;
SQ

Query Match 20.0%; Score 6; DB 2; Length 1870;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
DB 241 NCERTCT 246

RESULT 14
LMA2_HUMAN STANDARD; PRT; 3110 AA.
ID LMA2_HUMAN
AC P24043; Q14736; Q93022;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain).
GN Name=LMA2; Synonyms=LMM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94124633; PubMed=8294519; DOI=10.1083/jcb.124.3.381;
RA Hvotlenho R., Niesinen M., Sainio K., Byers M., Eddy R., Hirvonen H., Shows T.B., Sariola H., Engvall E., Trygvason K.;
RT "Human laminin M chain (merosin): complete primary structure, chromosomal assignment, and expression of the M and A chain in human fetal tissues";
RL J. Cell Biol. 124:381-394(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=97066955; PubMed=8910357; DOI=10.1074/jbc.271.44.27664;
RA Zhang X., Hvotlenho R., Trygvason K.;
RT "Structure of the human laminin alpha2-chain gene (LMA2), which is affected in congenital muscular dystrophy";
RL J. Biol. Chem. 271:27664-27669(1996).
RN [3]
RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=90238994; PubMed=2185464;
RA Errig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E.;
RT "Merosin, a tissue-specific basement membrane protein, is a laminin-like protein";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
RN [4]
RP VARIANTS Gln-545; His-619; Leu-919; His-2586 AND Lys-2614.
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z., Marzluft G.A., Amato A.A., Mendell J.R.;
RT "Novel single base polymorphisms and rare sequence variants in the laminin 2-chain coding region detected by RNA/SSCP analysis";
RL Hum. Mutat. 13:174-174(1999).
RN [5]
RP ERRATUM.
RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z., Marzluft G.A., Amato A.A., Mendell J.R.;
RL Hum. Mutat. 13:340-340(1999).
RN [6]
RP VARIANT MDCL PRO-2564.
RX MEDLINE=21476011; PubMed=11591858;
RA He Y., Jones K.J., Vignier N., Morgan G., Chevallay M., Barois A., Raebourne-Machaud B., Hori H., Mizuta T., Tome F.M.S., North K.N., Guicheney P.;
RT "Congenital muscular dystrophy with primary partial laminin alpha-2 chain deficiency: molecular study";
RL Neurology 57:1319-1322(2001).
RN [7]
RP VARIANTS MDCL TYR-527 AND ARG-862.
RX MEDLINE=22439669; PubMed=12552556; DOI=10.1002/humu.10157;

RA Tezak Z., Prandini P., Boscaro M., Marin A., Devaney J., Marino M.,
RA Fanin M., Trevisan C.P., Park J., Tyson W., Finkel R., Garcia C.,
RA Angelini C., Hoffman E.P., Pegoraro E.;
RT "Clinical and molecular study in congenital muscular dystrophy with partial laminin alpha-2 (LMA2) deficiency";
RL Hum. Mutat. 21:103-111(2003).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin is thought to mediate the attachment, migration and organization of cells into tissues during embryonic development by interacting with other extracellular matrix components.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three different polypeptide chains (alpha, beta, gamma), which are bound to each other by disulfide bonds into a cross-shaped molecule comprising one long and three short arms with globular at each end. The alpha-2 chain is a subunit of laminin-2 (merosin) and laminin-4 (5-merosin).
CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement membranes (major component).
CC -1- TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve, cardiac muscle, pancreas, lung, spleen, kidney, adrenal gland, skin, testis, meninges, choroid plexus, and some other regions of the brain; not in liver, thymus and bone.
CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact with other laminin chains to form a coiled coil structure.
CC -1- DOMAIN: Domains VI, IV and G are globular.
CC -1- DISEASE: Defects in LMA2 are the cause of merosin-deficient congenital muscular dystrophy type 1A (MDCL) [MIM:607855]. MDCL is characterized by difficulty walking, hypotonia, proximal weakness, hyporeflexia, and white matter hypodensity on MRI.
CC -1- SIMILARITY: Contains 17 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 5 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 1 laminin IV domains.
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z26653; CAAB1394.1; -;
DR EMBL; U66796; AAB18388.1; JOINED.
DR EMBL; U66733; AAB18388.1; JOINED.
DR EMBL; U66734; AAB18388.1; JOINED.
DR EMBL; U66735; AAB18388.1; JOINED.
DR EMBL; U66736; AAB18388.1; JOINED.
DR EMBL; U66737; AAB18388.1; JOINED.
DR EMBL; U66738; AAB18388.1; JOINED.
DR EMBL; U66739; AAB18388.1; JOINED.
DR EMBL; U66740; AAB18388.1; JOINED.
DR EMBL; U66741; AAB18388.1; JOINED.
DR EMBL; U66742; AAB18388.1; JOINED.
DR EMBL; U66743; AAB18388.1; JOINED.
DR EMBL; U66744; AAB18388.1; JOINED.
DR EMBL; U66745; AAB18388.1; JOINED.
DR EMBL; U66746; AAB18388.1; JOINED.
DR EMBL; U66747; AAB18388.1; JOINED.
DR EMBL; U66748; AAB18388.1; JOINED.
DR EMBL; U66749; AAB18388.1; JOINED.
DR EMBL; U66750; AAB18388.1; JOINED.
DR EMBL; U66751; AAB18388.1; JOINED.
DR EMBL; U66752; AAB18388.1; JOINED.
DR EMBL; U66753; AAB18388.1; JOINED.
DR EMBL; U66754; AAB18388.1; JOINED.
DR EMBL; U66755; AAB18388.1; JOINED.
DR EMBL; U66756; AAB18388.1; JOINED.
DR EMBL; U66757; AAB18388.1; JOINED.
DR EMBL; U66758; AAB18388.1; JOINED.
DR EMBL; U66759; AAB18388.1; JOINED.
DR EMBL; U66760; AAB18388.1; JOINED.
DR EMBL; U66761; AAB18388.1; JOINED.
DR EMBL; U66762; AAB18388.1; JOINED.

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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:03:32 ; Search time 90.9818 seconds
(without alignments)
191.293 Million cell updates/sec

Title: US-09-977-406A-91

Perfect score: 45
Sequence: 1 EMQTDNCCTCTCYETEMQTD.....TCYETEMQTDNCCTCTCYET 45

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	45	100.0	45	AAO17998	AAO17998 Human PSP
2	45	100.0	60	AAO17999	AAO17999 Human PSP
3	30	66.7	30	AAO17997	AAO17997 Human PSP
4	16	35.6	16	AAO17917	AAO17917 Human pro
5	16	35.6	17	AAO17918	AAO17918 Human pro
6	16	35.6	18	AAO17919	AAO17919 Human pro
7	16	35.6	19	AAO17920	AAO17920 Human pro
8	16	35.6	20	AAO17921	AAO17921 Human pro
9	16	35.6	21	AAO17922	AAO17922 Human pro
10	16	35.6	22	AAO17923	AAO17923 Human pro
11	16	35.6	23	AAO17924	AAO17924 Human pro
12	16	35.6	24	AAO17925	AAO17925 Human pro
13	16	35.6	25	AAO17926	AAO17926 Human pro
14	16	35.6	26	AAO17927	AAO17927 Human pro
15	16	35.6	27	AAO17928	AAO17928 Human pro
16	16	35.6	28	AAO17929	AAO17929 Human pro
17	16	35.6	29	AAO17930	AAO17930 Human pro
18	16	35.6	30	AAO17931	AAO17931 Human pro
19	16	35.6	31	AAO17932	AAO17932 Human pro
20	16	35.6	32	AAO17933	AAO17933 Human pro
21	16	35.6	33	AAO17934	AAO17934 Human pro
22	16	35.6	34	AAO17935	AAO17935 Human pro
23	16	35.6	35	AAO17936	AAO17936 Human pro
24	16	35.6	36	AAO17937	AAO17937 Human pro
25	16	35.6	37	AAO17938	AAO17938 Human pro

26	16	35.6	38	AAO17939	AAO17939 Human pro
27	16	35.6	39	AAO17940	AAO17940 Human pro
28	16	35.6	40	AAO17941	AAO17941 Human pro
29	16	35.6	41	AAO17942	AAO17942 Human pro
30	16	35.6	42	AAO17943	AAO17943 Human pro
31	16	35.6	43	AAO17944	AAO17944 Human pro
32	16	35.6	44	AAO17945	AAO17945 Human pro
33	16	35.6	45	AAO17946	AAO17946 Human pro
34	16	35.6	46	AAO17947	AAO17947 Human pro
35	16	35.6	47	AAO17948	AAO17948 Human pro
36	16	35.6	48	AAO17949	AAO17949 Human pro
37	16	35.6	49	AAO17950	AAO17950 Human pro
38	16	35.6	50	AAO17951	AAO17951 Human pro
39	16	35.6	51	AAO17952	AAO17952 Human pro
40	16	35.6	52	AAO17953	AAO17953 Human pro
41	16	35.6	53	AAO17954	AAO17954 Human pro
42	16	35.6	54	AAO17955	AAO17955 Human pro
43	16	35.6	55	AAO17956	AAO17956 Human pro
44	16	35.6	56	AAO17957	AAO17957 Human pro
45	16	35.6	57	AAO17958	AAO17958 Human pro

ALIGNMENTS

RESULT 1
ID AAO17998 standard; protein; 45 AA.
XX
AC AAO17998;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human PSP94 analogue adaptor peptide #2.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
OS Synthetic.
XX
PN W0200233090-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001MO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S; Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
XX
DR New human prostate secretory protein of 94 amino acids, useful for
XX inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
XX PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Disclosure; Page 106; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of PSH. The
CC present sequence is an adaptor peptide useful in the invention

XX Sequence 45 AA;
SQ

Query Match 100.0%; Score 45; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCETCTCYETEMQTDNCETCTCYETEMQTDNCETCTCYET 45
DB 1 EMQTDNCETCTCYETEMQTDNCETCTCYETEMQTDNCETCTCYET 45

RESULT 2

AAO17999

ID AAO17999 standard; protein; 60 AA.

AC AAO17999;

XX 30-AUG-2002 (first entry)

DE Human PSP94 analogue adaptor peptide #3.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.

XX Synthetic.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Disclosure; Page 106; 185pp; English.

XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an adaptor peptide useful in the invention

XX Sequence 60 AA.

Query Match 100.0%; Score 45; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 3.2e-43;

Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCETCTCYETEMQTDNCETCTCYETEMQTDNCETCTCYET 45
DB 1 EMQTDNCETCTCYETEMQTDNCETCTCYETEMQTDNCETCTCYET 45

RESULT 3

AAO17997
ID AAO17997 standard; peptide; 30 AA.

AC AAO17997;

XX 30-AUG-2002 (first entry)

DE Human PSP94 analogue adaptor peptide #1.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.

XX Synthetic.

XX WO200233090-A2.

XX 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

XX 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

XX WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Disclosure; Page 105; 185pp; English.

XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an adaptor peptide useful in the invention

XX Sequence 30 AA;

Query Match 66.7%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCETCTCYETEMQTDNCETCTCYET 30
DB 1 EMQTDNCETCTCYETEMQTDNCETCTCYET 30

RESULT 4

AAO17917

ID AAO17917 standard; peptide; 16 AA.

AC AAO17917;

XX 30-AUG-2002 (first entry)

DE Human prostate secretory protein of 94 amino acids PSP94 analogue #6.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

KM benign prostate hyperplasia; cytostatic.
 XX Homo sapiens.
 OS
 XX
 XX W0200233090-A2.
 PN
 XX
 XX 25-APR-2002.
 PD
 XX
 XX 15-OCT-2001; 2001WO-CA001463.
 PF
 XX
 XX 16-OCT-2000; 2000CA-02321256.
 PR
 XX 20-AUG-2001; 2001CA-02355334.
 XX
 XX (PROC-) PROCYON BIOPHARMA INC.
 PA
 XX
 XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 PI
 XX WPI; 2002-471401/50.
 DR
 XX
 XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 CC
 XX
 XX Claim 2; Page 76; 185pp; English.
 PS
 XX
 XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 CC
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 35.6%; Score 16; DB 5; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMQTDNCETCTCYETE 16
 Db 1 EMQTDNCETCTCYETE 16
 RESULT 5
 ID AAO17918 standard; peptide; 17 AA.
 AC AAO17918;
 XX
 XX 30-AUG-2002 (first entry)
 DT
 XX
 XX Human prostate secretory protein of 94 amino acids PSP94 analogue #7.
 DE
 XX
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
 KM beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostate hyperplasia; cytostatic.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 XX W0200233090-A2.
 PN
 XX
 XX 25-APR-2002.
 PD
 XX
 XX 15-OCT-2001; 2001WO-CA001463.
 PF
 XX
 XX 16-OCT-2000; 2000CA-02321256.
 PR
 XX 20-AUG-2001; 2001CA-02355334.
 XX

PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 PI
 XX WPI; 2002-471401/50.
 DR
 XX
 XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 CC
 XX
 XX Claim 2; Page 76; 185pp; English.
 PS
 XX
 XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPI) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 CC
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 35.6%; Score 16; DB 5; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.2e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMQTDNCETCTCYETE 16
 Db 1 EMQTDNCETCTCYETE 16
 RESULT 6
 ID AAO17919 standard; peptide; 18 AA.
 AC AAO17919;
 XX
 XX 30-AUG-2002 (first entry)
 DT
 XX
 XX Human prostate secretory protein of 94 amino acids PSP94 analogue #8.
 DE
 XX
 XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPI; beta-MSP;
 KM beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostate hyperplasia; cytostatic.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 XX W0200233090-A2.
 PN
 XX
 XX 25-APR-2002.
 PD
 XX
 XX 15-OCT-2001; 2001WO-CA001463.
 PF
 XX
 XX 16-OCT-2000; 2000CA-02321256.
 PR
 XX 20-AUG-2001; 2001CA-02355334.
 XX
 XX (PROC-) PROCYON BIOPHARMA INC.
 PA
 XX
 XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
 PI
 XX WPI; 2002-471401/50.
 DR
 XX
 XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 CC
 XX
 XX Claim 2; Page 77; 185pp; English.
 PS
 XX
 XX The present invention relates to analogues of the human prostate

CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemionoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 18 AA;
Query Match 35.6%; Score 16; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQTDNCETCTCYETE 16
Db 1 EMQTDNCETCTCYETE 16
RESULT 7
AAOI7920
ID AAOI7920 standard; peptide; 19 AA.
XX
AC AAOI7920;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #9.
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
KW beta-microsemionoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KM benign prostatic hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200233090-A2.
PN
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
PI WPI; 2002-471401/50.
DR
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 77; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemionoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 19 AA;
Query Match 35.6%; Score 16; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQTDNCETCTCYETE 16
Db 1 EMQTDNCETCTCYETE 16
RESULT 8
AAOI7921
ID AAOI7921 standard; peptide; 20 AA.
XX
AC AAOI7921;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #10.
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
KW beta-microsemionoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KM benign prostatic hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX WO200233090-A2.
PN
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
PI WPI; 2002-471401/50.
DR
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 77; 185pp; English.
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemionoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 20 AA;
Query Match 35.6%; Score 16; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQTDNCETCTCYETE 16
Db 1 EMQTDNCETCTCYETE 16
RESULT 9
AAOI7922
ID AAOI7922 standard; peptide; 21 AA.
XX
AC AAOI7922;
XX

DT 30-AUG-2002 (first entry)
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #11.
DE
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KM benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX W0200233090-A2.
PN
XX
XX 25-APR-2002.
PD
XX
XX 15-OCT-2001; 2001MO-CA001463.
PF
XX 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
DR
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 78; 185pp; English.
PS
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
XX Sequence 21 AA;
SQ
Query Match 35.6%; Score 16; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16
RESULT 10
AAO17923 standard; peptide; 22 AA.
XX
XX AAO17923;
AC
XX
XX 30-AUG-2002 (first entry)
DT
XX
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #12.
DE
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KM benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX W0200233090-A2.
PN

XX
PD 25-APR-2002.
XX
XX 15-OCT-2001; 2001MO-CA001463.
PF
XX 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
DR
XX
XX New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
XX Claim 2; Page 78; 185pp; English.
PS
XX
XX The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (bets-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
XX Sequence 22 AA;
SQ
Query Match 35.6%; Score 16; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16
RESULT 11
AAO17924 standard; peptide; 23 AA.
XX
XX AAO17924;
AC
XX
XX 30-AUG-2002 (first entry)
DT
XX
XX Human prostate secretory protein of 94 amino acids PSP94 analogue #13.
DE
XX
XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KM benign prostate hyperplasia; cytostatic.
XX
XX Homo sapiens.
OS
XX W0200233090-A2.
PN
XX
XX 25-APR-2002.
PD
XX
XX 15-OCT-2001; 2001MO-CA001463.
PF
XX 16-OCT-2000; 2000CA-02321256.
PR 20-AUG-2001; 2001CA-02355334.
XX
XX (PROC-) PROCYON BIOPHARMA INC.
PA
XX Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX WPI; 2002-471401/50.
DR

RESULT 14

AA017927 standard; peptide; 26 AA.

AA017927;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94 analogue #16.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-microseminoprotein; human seminal plasma inhibin; analogue;

stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

benign prostate hyperplasia; cytostatic.

Homo sapiens.

WO200233090-A2.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 79; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP)). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 26 AA;

Query Match 35.6%; Score 16; DB 5; Length 26;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

KM beta-microseminoprotein; human seminal plasma inhibin; analogue;

KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

KM benign prostate hyperplasia; cytostatic.

Homo sapiens.

WO200233090-A2.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 79; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP)). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 27 AA;

Query Match 35.6%; Score 16; DB 5; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.8e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

1 EMQDNCETCTCYETE 16

Search completed: May 4, 2005, 14:25:11

Job time : 90.9818 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:13:33 ; Search time 23.0727 Seconds
(without alignments)
145.592 Million cell updates/sec

Title: US-09-977-406A-91

Perfect score: 45
Sequence: 1 EMQTDNCCTCYETEMQTD.....TCYETEMQTDNCCTCYET 45

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: Issued Patents AA:*
- 2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	35.6	94	US-07-899-535A-1	Sequence 1, Appli
2	16	35.6	114	US-09-513-999C-7807	Sequence 7807, Ap
3	6	13.3	241	US-08-460-309-17	Sequence 17, Appl
4	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
5	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
6	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
7	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
8	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
9	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
10	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
11	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
12	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
13	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
14	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
15	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
16	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
17	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
18	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
19	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
20	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
21	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
22	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
23	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
24	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
25	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
26	6	13.3	241	US-08-125-077-17	Sequence 17, Appl
27	6	13.3	241	US-08-125-077-17	Sequence 17, Appl

28	5	11.1	110	4	US-09-513-999C-7055	Sequence 7055, Ap
29	5	11.1	188	4	US-09-270-767-61692	Sequence 61692, A
30	5	11.1	192	3	US-08-685-466C-4	Sequence 4, Appli
31	5	11.1	230	4	US-09-248-796A-21826	Sequence 21826, A
32	5	11.1	231	4	US-09-265-540E-4	Sequence 4, Appli
33	5	11.1	243	2	US-08-460-309-15	Sequence 15, Appli
34	5	11.1	243	2	US-08-460-309-15	Sequence 15, Appli
35	5	11.1	243	2	US-08-125-077-15	Sequence 15, Appli
36	5	11.1	243	2	US-08-125-077-15	Sequence 15, Appli
37	5	11.1	259	4	US-09-328-352-5038	Sequence 5038, Ap
38	5	11.1	261	4	US-09-962-357-8	Sequence 8, Appli
39	5	11.1	314	1	US-08-486-036A-4	Sequence 4, Appli
40	5	11.1	314	3	US-09-005-298-4	Sequence 4, Appli
41	5	11.1	314	4	US-08-768-619-4	Sequence 4, Appli
42	5	11.1	314	5	PCT-US96-09848-4	Sequence 4, Appli
43	5	11.1	315	4	US-09-902-540-14527	Sequence 14527, A
44	5	11.1	316	1	US-08-482-282B-4	Sequence 4, Appli
45	5	11.1	316	4	US-09-543-681A-5873	Sequence 5873, Ap

ALIGNMENTS

RESULT 1
US-07-899-535A-1
Sequence 1, Application US/07899535A
Patent No. 5428011
GENERAL INFORMATION:
APPLICANT: Sheth, Anil R.
APPLICANT: Garde, Seema
TITLE OF INVENTION: Pharmaceutical Preparations For
TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Mr. George Loud
STREET: 2001 Jefferson Davis Highway, Suite 306
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,535A
FILING DATE: 16-JUN-1992
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Loud, George A.
REGISTRATION NUMBER: 25,814
REFERENCE/DOCKET NUMBER: SeB-A835
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-0960
TELEFAX: 703-415-0962
TELEX: 24 8614
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-07-899-535A-1
Query Match 35.6%; Score 16; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCYETE 16
|||
Db 31 EMQDNCCTCYETE 46

RESULT 2
US-09-513-999C-7807
Sequence 7807, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59 US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7807
LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -20..-1
OTHER INFORMATION: score 9
OTHER INFORMATION: seq VLFATFVTLGNA/SC
US-09-513-999C-7807

Query Match 35.6%; Score 16; DB 4; Length 114;
Best Local Similarity 100.0%; Pred.No. 8.4e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCCTCYETE 16
|||
Db 51 EMQDNCCTCYETE 66

RESULT 3
US-08-460-309-17
Sequence 17, Application US/08460309
Patent No. 5837496
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,309
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,077
FILING DATE: 22-SEP-1993
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-460-309-17

Query Match 13.3%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred.No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCCTCT 11
|||
Db 103 NCCTCT 108

RESULT 4
US-08-125-077-17
Sequence 17, Application US/08125077
Patent No. 5872231
GENERAL INFORMATION:
APPLICANT: Engvall, Eva
APPLICANT: Leivo, Ilmo
TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
TITLE OF INVENTION: Fragments and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,077
FILING DATE: 22-SEP-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US 94/10730
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-125-077-17

Query Match 13.3%: Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 103 NCERTCT 108

RESULT 5
US-09-248-796A-20514
Sequence 20514, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20514
LENGTH: 362
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20514

Query Match 13.3%: Score 6; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TEMQTD 20
Db 341 TEMQTD 346

RESULT 6
US-09-949-016-7517
Sequence 7517, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7517
LENGTH: 2123
TYPE: PRT
ORGANISM: Human
US-09-949-016-7517

Query Match 13.3%: Score 6; DB 4; Length 2123;
Best Local Similarity 100.0%; Pred. No. 59;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 NCERTCT 11
Db 405 NCERTCT 410

RESULT 7
US-09-961-403-7
Sequence 7, Application US/09961403
Patent No. 6780594
GENERAL INFORMATION:
APPLICANT: HB-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETZSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: REGIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 3070
TYPE: PRT
ORGANISM: Homo sapiens
US-09-961-403-7

Query Match 13.3%: Score 6; DB 4; Length 3070;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 8
US-09-562-702A-8
Sequence 8, Application US/09562702A
Patent No. 6632790
GENERAL INFORMATION:
APPLICANT: Yurchenco, Peter
TITLE OF INVENTION: Laminin 2 and Methods for Its Use
FILE REFERENCE: 99-274-B
CURRENT APPLICATION NUMBER: US/09/562,702A
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/155,945
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: 60/143,289
PRIOR FILING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/139,198
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/131,720
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 3088
TYPE: PRT
ORGANISM: Homo sapiens
US-09-562-702A-8

Query Match 13.3%: Score 6; DB 4; Length 3088;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
Db 367 NCERTCT 372

RESULT 9
US-09-562-702A-4
; Sequence 4, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-4

Query Match 13.3%; Score 6; DB 4; Length 3089;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
Db 367 NCERTCT 372

RESULT 10
US-09-562-702A-2
; Sequence 2, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-2

Query Match 13.3%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 11

US-09-562-702A-6
; Sequence 6, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-6

Query Match 13.3%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 12
US-09-561-709B-7
; Sequence 7, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgess, Robert
; APPLICANT: Champilaud, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Brunken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-7

Query Match 13.3%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NCERTCT 11
Db 389 NCERTCT 394

RESULT 13
US-09-917-254-86
; Sequence 86, Application US/09917254
; Patent No. 6703204

GENERAL INFORMATION:
 APPLICANT: Mutter, George
 TITLE OF INVENTION: Prognostic Classification of Breast Cancer
 FILE REFERENCE: B0801/7224 (URV)
 CURRENT FILING DATE: 2001-07-27
 PRIOR APPLICATION NUMBER: US 60/222,093
 PRIOR FILING DATE: 2000-07-28
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: Patent version 3.0
 SEQ ID NO: 86
 LENGTH: 3110
 TYPE: PRT
 ORGANISM: Homo Sapiens
 US-09-917-254-86

Query Match 13.3%; Score 6; DB 4; Length 3110;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
 Db 389 NCERTCT 394

RESULT 14
 US-09-949-016-5937
 Sequence 5937, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 5937
 LENGTH: 3110
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-5937

Query Match 13.3%; Score 6; DB 4; Length 3110;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
 Db 389 NCERTCT 394

RESULT 15
 US-08-460-309-4
 Sequence 4, Application US/08460309
 Patent No. 5837496
 GENERAL INFORMATION:
 APPLICANT: Enyvall, Eva
 TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
 Fragments and Uses Thereof
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,309
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/125,077
 FILING DATE: 22-SEP-1993
 APPLICATION NUMBER: US PCT/US 94/10730
 FILING DATE: 21-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/472,319
 FILING DATE: 30-JAN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/919,951
 FILING DATE: 27-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9721
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-460-309-4

Query Match 13.3%; Score 6; DB 2; Length 3111;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
 Db 389 NCERTCT 394

Search completed: May 4, 2005, 14:37:24
 Job time: 23.0727 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:33:36 ; Search time 50.2364 Seconds
(without alignments)
298.385 Million cell updates/sec

Title: US-09-977-406A-91

Perfect score: 45
Sequence: 1 EMQDNCETCTCYETEMQTD.....TCYETEMQDNCETCTCYET 45

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Gapop 60.0 , Gapext 60.0

Searched: 1426032 seqs, 333106140 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	45	100.0	60	10	US-09-977-406A-92
3	30	66.7	30	10	US-09-977-406A-90
4	16	35.6	16	10	US-09-977-406A-10
5	16	35.6	17	10	US-09-977-406A-11
6	16	35.6	18	10	US-09-977-406A-12
7	16	35.6	19	10	US-09-977-406A-13
8	16	35.6	20	10	US-09-977-406A-14
9	16	35.6	21	10	US-09-977-406A-15
10	16	35.6	22	10	US-09-977-406A-16
11	16	35.6	23	10	US-09-977-406A-17
12	16	35.6	24	10	US-09-977-406A-18
13	16	35.6	25	10	US-09-977-406A-19

14	16	35.6	26	10	US-09-977-406A-20	Sequence 20, Appl
15	16	35.6	27	10	US-09-977-406A-21	Sequence 21, Appl
16	16	35.6	28	10	US-09-977-406A-22	Sequence 22, Appl
17	16	35.6	29	10	US-09-977-406A-23	Sequence 23, Appl
18	16	35.6	30	10	US-09-977-406A-24	Sequence 24, Appl
19	16	35.6	31	10	US-09-977-406A-25	Sequence 25, Appl
20	16	35.6	32	10	US-09-977-406A-26	Sequence 26, Appl
21	16	35.6	33	10	US-09-977-406A-27	Sequence 27, Appl
22	16	35.6	34	10	US-09-977-406A-28	Sequence 28, Appl
23	16	35.6	35	10	US-09-977-406A-29	Sequence 29, Appl
24	16	35.6	36	10	US-09-977-406A-30	Sequence 30, Appl
25	16	35.6	37	10	US-09-977-406A-31	Sequence 31, Appl
26	16	35.6	38	10	US-09-977-406A-32	Sequence 32, Appl
27	16	35.6	39	10	US-09-977-406A-33	Sequence 33, Appl
28	16	35.6	40	10	US-09-977-406A-34	Sequence 34, Appl
29	16	35.6	41	10	US-09-977-406A-35	Sequence 35, Appl
30	16	35.6	42	10	US-09-977-406A-36	Sequence 36, Appl
31	16	35.6	43	10	US-09-977-406A-37	Sequence 37, Appl
32	16	35.6	44	10	US-09-977-406A-38	Sequence 38, Appl
33	16	35.6	45	10	US-09-977-406A-39	Sequence 39, Appl
34	16	35.6	46	10	US-09-977-406A-40	Sequence 40, Appl
35	16	35.6	47	10	US-09-977-406A-41	Sequence 41, Appl
36	16	35.6	48	10	US-09-977-406A-42	Sequence 42, Appl
37	16	35.6	49	10	US-09-977-406A-43	Sequence 43, Appl
38	16	35.6	50	10	US-09-977-406A-44	Sequence 44, Appl
39	16	35.6	51	10	US-09-977-406A-45	Sequence 45, Appl
40	16	35.6	52	10	US-09-977-406A-46	Sequence 46, Appl
41	16	35.6	53	10	US-09-977-406A-47	Sequence 47, Appl
42	16	35.6	54	10	US-09-977-406A-48	Sequence 48, Appl
43	16	35.6	55	10	US-09-977-406A-49	Sequence 49, Appl
44	16	35.6	56	10	US-09-977-406A-50	Sequence 50, Appl
45	16	35.6	57	10	US-09-977-406A-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1
US-09-977-406A-91
Sequence 91, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-91

Query Match 100.0%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.9e+43;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 EMQDNCETCTCYETEMQDNCETCTCYETEMQDNCETCTCYET 45
Db 1 EMQDNCETCTCYETEMQDNCETCTCYETEMQDNCETCTCYET 45

RESULT 2
US-09-977-406A-92
Sequence 92, Application US/09977406A

Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 92
LENGTH: 60
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-92

Query Match 100.0%; Score 45; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 5e-43;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 EMQDNCETCTCYETEMQDNCETCTCYETEMQDNCETCTCYET 45

RESULT 3
US-09-977-406A-90
Sequence 90, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 90
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-90

Query Match 66.7%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
DB 1 EMQDNCETCTCYETEMQDNCETCTCYET 30

RESULT 4
US-09-977-406A-10
Sequence 10, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-10

Query Match 35.6%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 5
US-09-977-406A-11
Sequence 11, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-11

Query Match 35.6%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 6
US-09-977-406A-12
Sequence 12, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12

LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-12

Query Match 35.6%; Score 16; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
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Db 1 EMQDNCETCTCYETE 16

RESULT 7
US-09-977-406A-13
Sequence 13, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-13

Query Match 35.6%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||||
Db 1 EMQDNCETCTCYETE 16

RESULT 8
US-09-977-406A-14
Sequence 14, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-14

Query Match 35.6%; Score 16; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
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Db 1 EMQDNCETCTCYETE 16

RESULT 9
US-09-977-406A-15
Sequence 15, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-15

Query Match 35.6%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||||
Db 1 EMQDNCETCTCYETE 16

RESULT 10
US-09-977-406A-16
Sequence 16, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-16

Query Match 35.6%; Score 16; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||||
Db 1 EMQDNCETCTCYETE 16

RESULT 11
US-09-977-406A-17
; Sequence 17, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-17

Query Match 35.6%; Score 16; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCETCTCYETE 16
|||
Db 1 EMQTDNCETCTCYETE 16

RESULT 12
US-09-977-406A-18
; Sequence 18, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-18

Query Match 35.6%; Score 16; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCETCTCYETE 16
|||
Db 1 EMQTDNCETCTCYETE 16

RESULT 13
US-09-977-406A-19
; Sequence 19, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:

; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-19

Query Match 35.6%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCETCTCYETE 16
|||
Db 1 EMQTDNCETCTCYETE 16

RESULT 14
US-09-977-406A-20
; Sequence 20, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406A-20

Query Match 35.6%; Score 16; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCETCTCYETE 16
|||
Db 1 EMQTDNCETCTCYETE 16

RESULT 15
US-09-977-406A-21
; Sequence 21, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16

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; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ. ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ. ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rhuSP94 sequence (polypeptide analog)
US-09-977-406A-21

```

```

Query Match      35.6%; Score 16; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 EMQTDNCETCTCYETE 16
      |||||
Db      1 EMQTDNCETCTCYETE 16

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Search completed: May 4, 2005, 15:24:09
Job time : 51.2364 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:12:38 ; Search time 16.2 Seconds
(without alignments)
267.269 Million cell updates/sec

Title: US-09-977-406a-91

Perfect score: 45
Sequence: 1 EMQDNCFCCTCYETEMQD.....TCYETEMQDNCFCCTCYET 45

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	35.6	114	2 A34567	beta-microseminop
2	6	13.3	326	2 UC7094	nine-heme cytochro
3	6	13.3	601	2 B96744	unknown protein [i
4	6	13.3	895	2 T32374	hypothetical prote
5	6	13.3	1045	2 A29840	serine proteinase
6	5	11.1	38	2 JN0613	defensin 4K - scor
7	5	11.1	38	2 S27242	defensin - blue da
8	5	11.1	83	2 S53116	methionine adenosy
9	5	11.1	91	2 S52089	transcription fact
10	5	11.1	114	2 A54663	seminal plasma pro
11	5	11.1	119	1 S73864	hypothetical prote
12	5	11.1	127	2 E69429	conserved hypochet
13	5	11.1	130	2 G65019	hypothetical prote
14	5	11.1	155	2 F81108	toxin-activating p
15	5	11.1	167	2 C86241	protein T1685.9 [i
16	5	11.1	210	2 AC2316	transposase alpha08
17	5	11.1	226	2 C70962	hypothetical prote
18	5	11.1	246	2 A81679	conserved hypochet
19	5	11.1	256	2 T05554	hypothetical prote
20	5	11.1	281	2 A11064	probable outer mem
21	5	11.1	287	2 F96738	hypothetical prote
22	5	11.1	295	2 S6790	hypothetical prote
23	5	11.1	301	2 T26546	hypothetical prote
24	5	11.1	315	2 S66038	ycac protein - Bac
25	5	11.1	317	2 C83652	hypothetical prote
26	5	11.1	319	1 F50370	transcription fact
27	5	11.1	322	1 C90905	hypothetical prote
28	5	11.1	334	2 D82803	glyceraldehyde-3-p
29	5	11.1	339	2 T16273	hypothetical prote

30	5	11.1	340	1 B55973	transcription fact
31	5	11.1	347	2 AC0825	anaerobic sulfite
32	5	11.1	347	2 A38453	transcription fact
33	5	11.1	349	1 I50369	transcription fact
34	5	11.1	358	1 A55973	transcription fact
35	5	11.1	358	1 I51735	transcription fact
36	5	11.1	359	1 I51734	transcription fact
37	5	11.1	360	1 A55198	transcription fact
38	5	11.1	360	2 T06592	methionine adenosy
39	5	11.1	361	2 I50505	gene wnt8 protein
40	5	11.1	363	1 C55973	transcription fact
41	5	11.1	366	2 S66351	methionine adenosy
42	5	11.1	374	2 S41758	heat shock protein
43	5	11.1	374	2 C97058	molecular chaperon
44	5	11.1	385	2 G83817	coproporphyrinogen
45	5	11.1	390	2 S46540	methionine adenosy

ALIGNMENTS

RESULT 1
A34567
beta-microseminoprotein precursor - human
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma prot
C:Species: Homo sapiens (man)
C>Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 09-Jul-2004
C:Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682
R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
A:Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein g
A:Reference number: A34567; MUID:90211299; PMID:2322265
A:Accession: A34567
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-114 <GRE>
A:Cross-references: UNIPROT:P08118; GB:M34376; NID:G514370; PIDN:AA59871.1; PID:G514372
R:Mitkay, M.; Nolet, S.; Fournier, S.; Benjannet, S.; Chapdelaine, P.; Paradis, G.; Dube,
DNA 6, 23-29, 1987
A:Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma p
A:Reference number: A26451; MUID:87161231; PMID:3829888
A:Accession: A26451
A:Molecule type: mRNA
A:Residues: 1-114 <MBI>
A:Cross-references: GB:M15885; NID:G338414; PIDN:AA3635.1; PID:G338415
R:Akiyama, K.; Yoshioke, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Tsuda, R.; Hara, M
Biochim. Biophys. Acta 829, 288-294, 1985
A:Title: The amino acid sequence of human beta-microseminoprotein.
A:Reference number: A29777; MUID:85199974; PMID:3995056
A:Accession: A29777
A:Molecule type: Protein
A:Residues: 21-58, 'PT', 61-113 <AKI>
R:Seidah, N.G.; Arbatci, N.J.; Rochemont, J.; Sheth, A.R.; Chretien, M.
FEBS Lett. 175, 349-355, 1984
A:Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction of
A:Reference number: A30984; MUID:85004133; PMID:6434350
A:Accession: A30984
A:Molecule type: Protein
A:Residues: 21-112, 'G', 114 <SEI>
R:Weiber, H.; Anderson, C.; Murne, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
Am. J. Pathol. 117, 593-604, 1990
A:Title: Beta microseminoprotein is not a prostate-specific protein.
A:Reference number: A60673; MUID:90379237; PMID:2205059
A:Accession: A60673
A:Molecule type: Protein
A:Residues: 21, 'X', 23-34 <WEI>
R:Nolet, S.; Mitkay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A:Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16238
A:Molecule type: DNA

A/Residues: 1-114 <NOL>
 A/Cross-references: EMBL:X57928; NID:G35760; PIDN:CAA41002.1; PID:G825707
 A/Note: the authors translated the codon ACT for residue 54 as TTP
 R/Liu, A.Y.; Bradner, R.C.; Vessella, R.L.
 Cancer Lett. 74, 91-99, 1993
 A/Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.
 A/Reference number: 152682; MUID:94115955; PMID:7506990
 A/Accession: 152682
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-114 <RES>
 A/Cross-references: GB:S67815; NID:G460568; PIDN:AA29732.1; PID:G460569
 A/Comment: This protein is a component of seminal plasma as well as secretory fluids from
 C/Genetics:
 A/Gene: GDB:MSMB
 A/Cross-references: GDB:128042; OMIM:157145
 A/Map position: 10q11.2-10q11.2
 A/Introns: 1/3; 37/1; 72/2
 C/Superfamily: seminal plasma protein
 C/Keywords: semen
 F.1-20/Domains: signal sequence #status predicted <SIG>
 F.21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 35.6%; Score 16; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWQDNCCTCTCCTE 16
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 DB 51 EWQDNCCTCTCCTE 66

RESULT 2
 JCT094
 nine-heme cytochrome c - Desulfovibrio desulfuricans
 C/Species: Desulfovibrio desulfuricans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: JCT094
 R/Saraiya, L.M.; da Costa, P.N.; Legall, J.
 Biochem. Biophys. Res. Commun. 262, 629-634, 1999
 A/Title: Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774 nine-heme c
 A/Reference number: JCT094; MUID:99400423; PMID:10471375
 A/Accession: JCT094
 A/Molecule type: DNA
 A/Residues: 1-326 <SAR>
 A/Cross-references: UNIPROT:Q9RNE8; GB:AF186393; NID:G5924394; PIDN:AA25586.1; PID:G592
 A/Experimental source: ATCC 27774
 C/Genetics:
 A/Gene: 9HCC
 C/Keywords: electron transfer; heme; heme binding

Query Match 13.3%; Score 6; DB 2; Length 326;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 DNCCTC 10
 |||||
 DB 75 DNCCTC 80

RESULT 3
 B96744
 unknown protein [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: B96744
 R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Jensen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: B96744
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-601 <STO>
 A/Cross-references: UNIPROT:Q9C7H2; GB:AE005173; NID:G11054407; PIDN:AA27794.1; GSPDB:G
 C/Genetics:
 A/Gene: F28P5.4
 A/Map position: 1

Query Match 13.3%; Score 6; DB 2; Length 601;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CECTTC 12
 |||||
 DB 514 CECTTC 519

RESULT 4
 T32374
 hypothetical protein K10F12.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
 C/Accession: T32374
 R/Wohlmann, P.; Beck, C.
 submitted to the EMBL Data Library, September 1997
 A/Description: The sequence of C. elegans cosmid K10F12.
 A/Reference number: Z21157
 A/Accession: T32374
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-895 <WOH>
 A/Cross-references: EMBL:AF025462; PIDN:AB71005.1; GSPDB:GN00021; CESP:K10F12.3
 A/Experimental source: strain Bristol NZ; clone K10F12
 C/Genetics:
 A/Gene: CESP:K10F12.3
 A/Map position: 3
 A/Introns: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 624
 C/Superfamily: yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phospho
 sphodiesterase domain Y homology
 F.338-487/Domains: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 13.3%; Score 6; DB 2; Length 895;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TDNCCT 9
 |||||
 DB 288 TDNCCT 293

RESULT 5
 A29840
 serine proteinase (EC 3.4.21.-) precursor - Serratia marcescens (strain IFO-3046)
 C/Species: Serratia marcescens
 C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C/Accession: A29840
 R/Yanagida, N.; Uozumi, T.; Bepko, T.
 J. Bacteriol. 166, 937-944, 1986
 A/Title: Specific excretion of Serratia marcescens protease through the outer membrane of
 A/Reference number: A29840; MUID:86223815; PMID:3011754
 A/Accession: A29840
 A/Molecule type: DNA
 A/Residues: 1-1045 <YAN>
 A/Cross-references: UNIPROT:P09489; GB:M13469; NID:G152857; PIDN:AA26572.1; PID:G152858
 C/Superfamily: autotransporter subunit-like protease precursor; subtilisin homology
 C/Keywords: hydrolase; serine proteinase
 F.1-27/Domains: signal sequence #status predicted <SIG>
 F.28-408/Product: serine proteinase #status predicted <MAT>

F:67-355/Domain: subtilisin homology <SBT>
F:409-1045/Domain: carboxyl-terminal propeptide #status predicted <PRO>
F:76,112,341/Active site: Asp, His, Ser #status predicted

Query Match 13.3%; Score 6; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TEMOTD 20
DB 953 TEMOTD 958

RESULT 6
JN0613
defensin 4K - scorpion (Leiurus quinquestriatus)
N/Alternate names: antibacterial 4K peptide
C/Species: Leiurus quinquestriatus hebraeus
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0613

R/Cociancich, S.; Goyffon, M.; Bontems, F.; Bulet, P.; Bouet, F.; Menez, A.; Hoffmann, J.
Biochem. Biophys. Res. Commun. 194, 17-22, 1993
A/Title: Purification and characterization of a scorpion defensin, a 4kDa antibacterial
A/Reference number: JN0613; MUID:93326112; PMID:8333834
A/Accession: JN0613

A/Molecule type: protein
A/Residues: 1-38 <COC>
A/Cross-references: UNIPROT:P41965
A/Note: this protein is similar to scorpion toxins and insect defensins

Query Match 11.1%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13
DB 32 TCTCY 36

RESULT 7
S27242
defensin - blue darner
C/Species: Aeschna cyanea (blue darner)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S27242

R/Bulet, P.; Cociancich, S.; Reuland, M.; Sauber, F.; Bischoff, R.; Hegy, G.; van Dorsselaere, J.
Biochem. Biophys. Res. Commun. 209, 977-984, 1992
A/Title: A novel insect defensin mediates the inducible antibacterial activity in larvae
A/Reference number: S27242; MUID:93049356; PMID:1425705
A/Accession: S27242

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-38 <BDL>
A/Cross-references: UNIPROT:P80154

Query Match 11.1%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TCTCY 13
DB 33 TCTCY 37

RESULT 8
S53116
methionine adenosyltransferase (EC 2.5.1.6) - chickpea (fragment)
N/Alternate names: S-adenosylmethionine synthetase
C/Species: Cicer arietinum (chickpea, garbanzo)
C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S53116
R/Cervantes, E.
submitted to the EMBL Data Library, March 1995

A/Reference number: S53116
A/Accession: S53116
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-83 <CER>
A/Cross-references: UNIPROT:Q39465; EMBL:X85252; NID:G1808591; PIDN:CAA59508.1; PID:9732
C/Species: Cicer arietinum (chickpea, garbanzo)
C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S53116
R/Cervantes, E.
submitted to the EMBL Data Library, March 1995

Query Match 11.1%; Score 5; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CECTC 11
DB 43 CECTC 47

RESULT 9
S52089
transcription factor isl-2a (clone S3) - chinook salmon
N/Alternate names: insulin enhancer-binding protein isl-2a; islet-2a protein
C/Species: Oncorhynchus tshawytscha (chinook salmon)
C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C/Accession: S52089

R/Gong, Z.; Hew, C.L.
Biochim. Biophys. Acta 1260, 349-354, 1995
A/Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynchus tshawytscha)
A/Reference number: S52089; MUID:95178560; PMID:7873614
A/Accession: S52089

A/Molecule type: mRNA
A/Residues: 1-91 <GON>
A/Cross-references: EMBL:X54882
A/Experimental source: clone S3
C/Genetics:

A/Gene: isl-2a
C/Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat h
C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulation
F:3-56/Domain: LIM metal-binding repeat homology <LIM>

Query Match 11.1%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ECTTC 12
DB 40 ECTTC 44

RESULT 10
A54663
seminal plasma protein PSP-94 precursor - rhesus macaque
N/Alternate names: prostatic secretory protein PSP94
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C/Accession: S16237; A54663

R/Nolet, S.; Mbikay, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A/Reference number: S16237; MUID:91274357; PMID:2054385
A/Accession: S16237

A/Molecule type: DNA
A/Residues: 1-114 <NO2>
A/Cross-references: UNIPROT:P25142; EMBL:X57932; NID:G38094; PIDN:CAA41003.1; PID:982915;
R/Nolet, S.; St-Louis, D.; Mbikay, M.; Chretien, M.
Genomics 9, 775-777, 1991

A/Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence bet
A/Reference number: A54663; MUID:91244325; PMID:2037304
A/Accession: A54663
A/Molecule type: mRNA
A/Residues: 1-114 <NO2>
A/Cross-references: GB:M92161; NID:G342280; PIDN:AAA36903.1; PID:G342281

C:Genetics:
A:Introns: 1/3, 37/1: 72/2
C:Superfamily: seminal plasma protein
F:1-20/Domain: signal sequence #status predicted <SIG>

Query Match 11.1%; Score 5; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8
DB 54 TDNCE 58

RESULT 11
S73864
hypothetical protein H10_orf119 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S73864
R:Himmelreich, R.; Hilbert, H.; Piagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73864
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-119 <HIM>
A:Cross-references: UNIPROT:P75480; EMBL:AE000052; GB:U00089; NID:G1674223; PIDN:AAB9618
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: holo-ACP synthase

Query Match 11.1%; Score 5; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTDNC 7
DB 21 QTDNC 25

RESULT 12
E69429
conserved hypothetical protein AFI438 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69429
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weisman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Unterbach, T.; Cotton, M.D.; Spriggs, T.; Ariciach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Moese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69429
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-127 <KLE>
A:Cross-references: UNIPROT:Q28834; GB:AE001004; GB:AE000782; NID:G2689327; PIDN:AAB9881

Query Match 11.1%; Score 5; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CYETE 16
DB 16 CYETE 20

RESULT 13
G65019
hypothetical protein b2448 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: G65019
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
; Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G65019
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-130 <BLAT>
A:Cross-references: UNIPROT:P76548; GB:AE000332; GB:U00096; NID:G1788789; PIDN:AAC75501.1
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli hypothetical protein b2448

Query Match 11.1%; Score 5; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8
DB 43 TDNCE 47

RESULT 14
F81108
toxin-activating protein, probable NMB1210 [imported] - Neisseria meningitidis (strain MC
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81108
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiogni, V.; Pizze, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <TEP>
A:Cross-references: UNIPROT:Q9JZB0; GB:AE002469; GB:AE002098; NID:G7226446; PIDN:AAF41597
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1210
C:Superfamily: hemolysin C

Query Match 11.1%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ETEWQ 18
DB 80 ETEWQ 84

RESULT 15
C86241
protein T16B5.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C86241
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C86241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-167 <STO>
A:Cross-references: UNIPROT:Q9SAC5; GB:AE005172; NID:94874271; PIDN:AAD31336.1; GSPDB:GN
C:Genetics:
A:Gene: TIGB5.9
A:Map position: 1

Query Match 11.1%; Score 5; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TCYET 15
|||
|||
Db 91 TCYET 95

Search completed: May 4, 2005, 14:34:57
Job time : 16.2 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:04:27 ; Search time 77.2364 Seconds

(without alignments)
298.351 Million cell updates/sec

Title: US-09-977-406a-91

Sequence: 1 EMQDNCCTCTCYETEMQTD.....TCYETEMQDNCCTCTCYET 45

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	35.6	114	1	MSMB_HUMAN
2	7	15.6	114	1	MSMB_PAPAN
3	6	13.3	196	2	Q9D8T1
4	6	13.3	215	2	Q7V5F4
5	6	13.3	326	1	CYC9_DESDE
6	6	13.3	459	1	MURD_LACPL
7	6	13.3	601	2	Q9C7H2
8	6	13.3	1045	1	PRTS_SERMA
9	6	13.3	1068	2	Q8IA76
10	6	13.3	1075	2	Q8IA75
11	6	13.3	1615	2	Q7QZU9
12	6	13.3	1870	2	Q7OH34
13	6	13.3	1870	2	Q9J5A0
14	6	13.3	3110	1	IMA2_HUMAN
15	5	11.1	37	1	DEF4_HUMAN
16	5	11.1	38	1	DEF4_LEIOH
17	5	11.1	38	1	DEF4_AESCY
18	5	11.1	51	2	Q7Y3N1
19	5	11.1	54	2	Q24985
20	5	11.1	58	2	Q8FCX2
21	5	11.1	70	2	Q8R5C3
22	5	11.1	74	1	DEF1_DERVA
23	5	11.1	74	2	Q86LE4
24	5	11.1	75	2	Q8JX66
25	5	11.1	75	2	Q8JX67
26	5	11.1	77	2	Q8CJL6
27	5	11.1	81	2	Q8VY76
28	5	11.1	83	2	Q9J465
29	5	11.1	105	2	Q8BU77
30	5	11.1	110	2	Q42169
31	5	11.1	111	2	Q9JH97

32	5	11.1	112	2	Q854B7	Q854B7 mycobacteri
33	5	11.1	113	2	Q22079	Q22079 nicotiana t
34	5	11.1	114	1	MSMB_MACMU	P25142 macaca mla
35	5	11.1	114	2	Q8L2F3	Q8L2F3 helicobacte
36	5	11.1	115	2	Q7KTX0	Q7KTX0 drosophila
37	5	11.1	117	2	Q8A7Y2	Q8A7Y2 bacteroides
38	5	11.1	119	1	ACPS_MYCPN	P75480 mycoplasma
39	5	11.1	121	2	Q7ZGB3	Q7ZGB3 human immun
40	5	11.1	127	2	Q28834	Q28834 archaeoglob
41	5	11.1	127	2	Q6IKD4	Q6IKD4 drosophila
42	5	11.1	130	1	YFQ_ECOLI	YFQ_ECOLI escherichia
43	5	11.1	131	2	Q8CFP4	Q8CFP4 mus musculus
44	5	11.1	132	2	Q97442	Q97442 giardia lam
45	5	11.1	133	2	Q6PRE3	Q6PRE3 helicobacte

ALIGNMENTS

RESULT 1
MSMB_HUMAN STANDARD; PRT; 114 AA.
ID MSMB_HUMAN Q13125; Q9UC59;
AC P08118; P11999; Q13125; Q9UC59;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (prostate secreted seminal plasma
protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma
beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).
GN Name=MSMB; Synonyms=PRSP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=67161231; PubMed=382988;
RA Mbikay M., Nolet S., Rounier S., Benjannet S., Chapelaine P.,
Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidan N.G.,
Chretien M.;
RT "Molecular cloning and sequence of the cDNA for a 94-amino-acid
seminal plasma protein secreted by the human prostate.";
RT DNA 6:23-29(1987).
RL [2]
RN [2]
RP MEDLINE=91274357; PubMed=2054385; DOI=10.1016/0167-4781(91)90016-F;
RA Nolet S., Mbikay M., Chretien M.;
RT "Prostatic secretory protein PSP94: gene organization and promoter
sequence in rhesus monkey and human.";
RT Biochim. Biophys. Acta 1089:247-249(1991).
RL [3]
RN [3]
RP MEDLINE=90211299; PubMed=2322265;
RA Green C.B., Liu W.Y., Kwok S.C.M.;
RT "Cloning and nucleotide sequence analysis of the human beta-
microseminoprotein gene.";
RT Biochem. Biophys. Res. Commun. 167:1184-1190(1990).
RL [4]
RN [4]
RP MEDLINE=90073664; PubMed=2590204;
RA Uvaybeck M., Lindstrom C., Weiber H., Abrahamson P.-A., Lilja H.,
Lundwall A.;
RT "Molecular cloning of a small prostate protein, known as beta-
microseminoprotein, PSP94 or beta-inhibin, and demonstration of
transcripts in non-genital tissues.";
RT Biochem. Biophys. Res. Commun. 164:1310-1315(1989).
RL [5]
RN [5]
RP MEDLINE=94115955; PubMed=7506990; DOI=10.1016/0304-3835(93)90049-F;
RA Liu A.Y., Bradner R.C., Vessella R.L.;
RT "Decreased expression of prostatic secretory protein PSP94 in prostate
cancer.";

RL Cancer Lett. 74:91-99 (1993).
 RP [6]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=Prostate; PubMed=7566962;
 RC MEDLINE=9603256; PubMed=7566962;
 RC Xuan J.W., Chin J.L., Guo Y., Chambers A.F., Finkelmann M.A.,
 RA Clarke M.W.;
 RA "Alternative splicing of PSP94 (prostatic secretory protein of 94
 RT amino acids) mRNA in prostate tissue.";
 RL Oncogene 11:1041-1047(1995).
 RP [7]
 RP SEQUENCE FROM N.A.
 RA Bajjal-Gupta M., Clarke M.W.;
 RT "Prostate specific protein (PSP94) expression in a human endometrial
 RT cell line (KLE).";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RP [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schaller G.D.,
 RA Altschul S.F., Zeeberg B., Buehler K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA DiCicco G.L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stetler-O'M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunatirne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
 RA Buterfield J.S.N., Krzywicki M.J., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [9]
 RP SEQUENCE OF 2-72 FROM N.A.
 RA MEDLINE=99421644; PubMed=10491085;
 RA Maekinen M., Valtanen-Andre C., Lundwall A.;
 RT "New world, but not old world, monkeys carry several genes encoding
 RT beta-microseminoprotein.";
 RL Eur. J. Biochem. 264:407-414 (1999).
 RP [10]
 RP SEQUENCE OF 21-113.
 RA MEDLINE=9519974; PubMed=3995056; DOI=10.1016/0167-4838(95)90200-6;
 RA Atiyama K., Yoshida Y., Schmid K., Offner G.D., Troxler R.F.,
 RA Tsuda R., Hara M.;
 RL "The amino acid sequence of human beta-microseminoprotein.";
 RL Biochim. Biophys. Acta 829:288-294 (1985).
 RP [11]
 RP SEQUENCE OF 21-114.
 RA MEDLINE=95004133; PubMed=6434350; DOI=10.1016/0014-5793(84)80766-8;
 RA Seidah N.G., Arbach N.J., Rochemont J., Sheeh A.R., Chretien M.;
 RT "Complete amino acid sequence of human seminal plasma beta-inhibin.
 RT Prediction of post-Gln-Arg cleavage as a maturation site.";
 RL FEBS Lett. 175:349-355 (1984).
 RP [12]
 RP SEQUENCE OF 21-50 AND 113-114.
 RA MEDLINE=92028964; PubMed=1930222;
 RA Liang Z.G., Kanada M., Koide S.S.;
 RT "Structural identity of immunoglobulin binding factor and prostatic
 RT secretory protein of human seminal plasma.";
 RL Biochem. Biophys. Res. Commun. 180:356-359 (1991).
 RP [13]
 RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.
 RC TISSUE=Semen;
 RC MEDLINE=95401076; PubMed=7671139; DOI=10.1016/1357-2725(95)00021-G;
 RA Onkudo I., Tada T., Ochiai T., Ueyama H., Eimoto T., Sasaki M.;

```

RT      "Human seminal plasma beta-microseminoprotein: its purification,
RT      characterization, and immunohistochemical localization.",
RL      Int. J. Biochem. Cell Biol. 27:603-611(1995).
RN      [14].
RP      SEQUENCE OF 21-32.
RX      MEDLINE=2648993; PubMed=11788998;
RX      DOI=10.1002/1615-9861(200201)21:1<112::AID-PROT112.3.CO;2-E;
RA      Ghahoui B., Stalhobm B., Tagesson C., Lindahl M.;
RT      "Newly identified proteins in human nasal lavage fluid from non-
RT      smokers and smokers using two-dimensional gel electrophoresis and
RT      peptide mass fingerprinting.",
RL      Proteomics 2:112-120(2002).
CC      -1- SUBCELLULAR LOCATION: Secreted. Sperm surface.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=ppp94;
CC      Name=ppp94;
CC      IsoId=po6118-1; Sequence=Displayed;
CC      Name=pp57;
CC      IsoId=po6118-2; Sequence=VSP_003275, VSP_003276;
CC      -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,
CC      breast and penis. Also expressed in pancreas, esophagus, stomach,
CC      duodenum, colon, trachea, lung, salivary glands and fallopian
CC      tube. Psp94 is expressed in lung and breast, whereas pp57 is
CC      found in kidney and bladder.
CC      -1- MISCELLANEOUS: Specific receptors for this protein are found on
CC      spermatozoa and in the prostate.
CC      -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC      -1- CAUTION: Was originally thought to inhibit the secretion of FSH by
CC      pituitary cells.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      -----
DR      EMBL; M34376; AAB59871.1; JOINED.
DR      EMBL; M34373; AAB59871.1; JOINED.
DR      EMBL; M34374; AAB59871.1; JOINED.
DR      EMBL; M34375; AAB59871.1; JOINED.
DR      EMBL; M15885; AAB36635.1; -.
DR      EMBL; X57928; CAA41002.1; -.
DR      EMBL; X57929; CAA41002.1; JOINED.
DR      EMBL; X57930; CAA41002.1; JOINED.
DR      EMBL; X57931; CAA41002.1; JOINED.
DR      EMBL; X57932; AAB29732.1; -.
DR      EMBL; U22178; AAB32556.1; -.
DR      EMBL; U78976; AAB37355.1; -.
DR      EMBL; BC005257; AAB05257.1; -.
DR      EMBL; AJ133356; CAB39325.1; -.
DR      PIR; A34567; A34567.
DR      PIR; G01730; G01730.
DR      Genew; HGNC:7372; MSMB.
DR      H-InvDB; HIX008822; -.
DR      MIM; 157145; -.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0005634; C:nucleus; TAS.
DR      InterPro; IPR008735; Psp94.
DR      Pfam; PF05825; Psp94, 1.
KW      Alternative splicing; Direct protein sequencing; Polymorphism; Signal.
FT      CHAIN 1 20
FT      DISULFID 21 114 Beta-microseminoprotein.
FT      DISULFID 22 38 By similarity.
FT      DISULFID 57 93 By similarity.
FT      DISULFID 60 69 Or C-66 with C-70 (By similarity).
FT      DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT      DISULFID 84 107 By similarity.
FT      VARSPIC 37 77 KMDIDGNKHKPISEMOTNDCCTCTCEFTFISCTLTSPV
FT      --> MFLHLVMTITTKAESRRRTASISWMRRRTQRPVLV
FT      VNG (in isoform PSp57).
FT      /FTid=VSP_003275.

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FT VASAPLIC 78 114 Missing (in isoform PSP97).
FT /FTid=VSP_003276.
Query Match 35.6%; Score 16; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 3; Se-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMOTNCETCTCYETE 16
Db 51 EMOTNCETCTCYETE 66
RESULT 2
MSMB_PAPAN STANDARD; PRT; 114 AA.
AC Q28767;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
protein) (Prostate secretory protein PSP94) (PSP-94).
GN Name=MSMB; Synonyms=PSP94;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=97316893; PubMed=9174167;
RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Molkay M., Zhong R.,
RA Chin J.L.;
RT "Molecular cloning and gene expression analysis of PSP94 (prostate
secretory protein of 94 amino acids) in primates.";
RL DNA Cell Biol. 16:627-638(1997).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface. (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U49786; AAB62726.1; -
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
KM Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 114 Beta-microseminoprotein.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.
FT DISULFID 60 69 Or C-60 with C-70 (By similarity).
FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT DISULFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98BD CRC64;
Query March 15.6%; Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 WQDNCN 8
Db 52 WQDNCN 58
RESULT 3
Q9DBY1 PRELIMINARY; PRT; 196 AA.
AC Q9DBY1;

DT 01-JUN-2001 (TRENBERG, 17, Created)
DT 01-JUN-2001 (TRENBERG, 17, Last sequence update)
DT 25-OCT-2004 (TRENBERG, 28, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:1810020E01 product:hypothetical protein, full insert
DE sequence (RIKEN CDNA 1810020E01).
GN Name=1810020E01Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium;
RT "The FANTOM Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multichipillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiranoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasuoka T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki H., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Reinhold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shmolen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Miliady S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smalick D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maizumi M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK007559; BAB25107.1; -;
 DR EMBL: BC023171; AAH23171.1; -;
 DR MGD; MGI:1913521; 1810020E01R1k.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR009801; DUF1370.
 DR Pfam; PF07114; DUF1370; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 196 AA; 21539 MW; 994DF5E2251C5FEB CRC64;

Query Match 13.3%; Score 6; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
 DB 98 NCETCT 103

RESULT 4
 QYVF4 PRELIMINARY; PRT; 215 AA.
 AC QYVF4;
 DT 01-OCT-2003 (TREMblrel. 25, Created)
 DT 01-OCT-2003 (TREMblrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Bacterial regulatory proteins, AsnC family.
 GN OrderedCusNames=PT1607;
 OS Prochlorococcus marinus (strain MIT 9313).
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococaceae;
 OC Prochlorococcus.
 OX NCBI_Taxid=74547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
 RA Rood G., Fairmer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinner E.R., Chisholm S.W.;
 RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
 RT niche differentiation.";
 RT Nature 424:1042-1047(2003).
 RL EMBL: BX572099; CAE21782.1; -;
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 KM Complete proteome.
 SQ SEQUENCE 215 AA; 24165 MW; E663MA68A216D0C5 CRC64;

Query Match 13.3%; Score 6; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 YETEMQ 18
 DB 142 YETEMQ 147

RESULT 5
 CYC9 DESDE STANDARD; PRT; 326 AA.
 AC CYC9 DESDE
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Nine-heme cytochrome c precursor (9Hcc).
 OS Desulfotribrio desulfuricans.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfotribriales;
 OC Desulfotribriaceae; Desulfotribrio.
 OX NCBI_Taxid=876;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99400423; PubMed=10473375; DOI=10.1006/bbrc.1999.1238;
 RA Saraiya L.M., da Costa P.N., Legall J.;
 RT "Sequencing the gene encoding Desulfotribrio desulfuricans ATCC 27774
 RT nine-heme cytochrome c.";
 RT Biochem. Biophys. Res. Commun. 262:629-634(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=20022508; PubMed=10555582;
 RA Matias P.M., Saraiya L.M., Soares C.M., Coelho A.V., Legall J.,
 RA Carrondo M.A.;
 RT "Nine-haem cytochrome c from Desulfotribrio desulfuricans ATCC 27774:
 RT primary sequence determination, crystallographic refinement at 1.8 Å
 RT and modelling studies of its interaction with the tetrahaem cytochrome
 RT c3.";
 RT J. Biol. Inorg. Chem. 4:478-494(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99148120; PubMed=10368280; DOI=10.1016/S0969-2126(99)80019-7;
 RA Matias P.M., Coelho R., Pereira I.A.C., Coelho A.V., Thompson A.W.,
 RA Sieker L., Legall J., Carrondo M.A.;
 RT "The primary and three-dimensional structures of a nine-haem
 RT cytochrome c from Desulfotribrio desulfuricans ATCC 27774 reveal a new
 RT member of the Hmc family.";
 RT Structure 7:119-130(1999).
 CC -1- FUNCTION: May form part of a transmembrane redox complex through
 CC which electrons are transferred to the cytoplasm for reduction of
 CC sulfate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- DOMAIN: Arranged into two tetraheme clusters and the extra heme 4
 CC is located asymmetrically between the two regions.
 CC -1- PTM: Binds 9 heme groups per subunit.
 CC -1- SIMILARITY: Contains 9 cytochrome c domains.
 CC -----
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 CC -----
 DR EMBL: AF186393; AAD56586.1; -;
 DR PIR: J07094; J07094.
 DR PDB: 19HC; X-ray; A/B=31-322.
 DR PDB: 10FW; X-ray; A/B=31-326.

PDB: 1OFY; X-ray; A/B=31-326.
 DR InterPro: IPR000345; CytC_heme_BS.
 DR InterPro: IPR002322; CytC_GIII.
 DR InterPro: IPR011031; Multihem_cyt.
 DR Pfam: PF02085; Cytochrom_cIII; 1.
 DR PRINTS: PRO0609; CYTOCHROME_C3.
 DR PROSITE: PS51008; MULTIHEME_CYT_C; 1.
 DR 3D-structure; Electron transport; Heme; Periplasmic; Repeat; Signal.
 KM SIGNAL 1 30
 FT CHAIN 1 30
 FT METAL 31 326 Nine-heme cytochrome C.
 FT METAL 67 70 Iron (heme 1 axial ligand).
 FT BINDING 77 77 Iron (heme 3 axial ligand).
 FT METAL 80 80 Heme 1 (covalent).
 FT BINDING 81 81 Iron (heme 1 axial ligand).
 FT METAL 82 82 Iron (heme 2 axial ligand).
 FT BINDING 89 89 Heme 2 (covalent).
 FT METAL 92 92 Heme 2 (covalent).
 FT BINDING 93 93 Iron (heme 2 axial ligand).
 FT METAL 111 111 Iron (heme 5 axial ligand).
 FT BINDING 127 127 Heme 3 (covalent).
 FT METAL 130 130 Heme 3 (covalent).
 FT BINDING 131 131 Iron (heme 3 axial ligand).
 FT METAL 141 141 Heme 4 (covalent).
 FT BINDING 144 144 Heme 4 (covalent).
 FT METAL 145 145 Iron (heme 4 axial ligand).
 FT BINDING 157 157 Heme 5 (covalent).
 FT METAL 160 160 Heme 5 (covalent).
 FT BINDING 161 161 Iron (heme 5 axial ligand).
 FT METAL 227 227 Iron (heme 6 axial ligand).
 FT METAL 230 230 Iron (heme 6 axial ligand).
 FT METAL 248 248 Iron (heme 8 axial ligand).
 FT BINDING 255 255 Heme 6 (covalent).
 FT BINDING 258 258 Heme 6 (covalent).
 FT METAL 259 259 Iron (heme 6 axial ligand).
 FT METAL 260 260 Iron (heme 7 axial ligand).
 FT BINDING 271 271 Heme 7 (covalent).
 FT METAL 274 274 Heme 7 (covalent).
 FT BINDING 275 275 Iron (heme 7 axial ligand).
 FT METAL 294 294 Iron (heme 9 axial ligand).
 FT BINDING 297 297 Heme 8 (covalent).
 FT METAL 300 300 Heme 8 (covalent).
 FT METAL 301 301 Iron (heme 8 axial ligand).
 FT METAL 314 314 Heme 9 (covalent).
 FT BINDING 317 317 Heme 9 (covalent).
 FT METAL 318 318 Heme 9 (heme 9 axial ligand).
 FT STRAND 43 46
 FT TURN 55 56
 FT STRAND 63 66
 FT METAL 67 73
 FT BINDING 77 80
 FT TURN 82 83
 FT METAL 89 91
 FT TURN 92 92
 FT METAL 99 101
 FT TURN 102 103
 FT METAL 106 111
 FT BINDING 127 137
 FT METAL 139 142
 FT TURN 143 143
 FT METAL 144 147
 FT BINDING 154 160
 FT STRAND 161 161
 FT TURN 165 166
 FT METAL 169 177
 FT TURN 178 178
 FT METAL 182 195
 FT TURN 204 206
 FT STRAND 211 213
 FT TURN 215 216
 FT STRAND 220 220
 FT STRAND 223 225
 FT METAL 227 236

FT TURN 237 240
 FT METAL 242 247
 FT TURN 251 257
 FT METAL 253 257
 FT TURN 258 258
 FT METAL 271 274
 FT TURN 281 282
 FT METAL 284 285
 FT TURN 289 303
 FT METAL 304 305
 FT TURN 311 312
 FT STRAND 320 320
 SQ SEQUENCE 326 AA; 35025 MW; 2ED7025ADDF250E3 CRC64;
 Query Match 13.3%; Score 6; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 DNCETC 10
 Db 75 DNCETC 80
 RESULT 6
 MURD_IACPL STANDARD; PRT; 459 AA.
 AC Q86V80;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase (EC 6.3.2.9) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid adding enzyme).
 DE Name=murd; OrderedLocNames=lp_2197;
 GN Lactobacillus plantarum.
 OS Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxId=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFSL1;
 RX MEDLINE=22480296; Pubmed=12565666; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M., Fiers W.M.E.J., Stekema W., Klein Lankhorst R.M., Bron P.A., Hofer W.M., Sietzen R.J., Kerkhoven R., De Vries M., Ursing B., De Vos W.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B., Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 RL "Complete genome sequence of Lactobacillus plantarum WCFSL1";
 CC -1- FUNCTION: Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (DMA) (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
 CC -1- PATHWAY: peptidoglycan biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the murDGP family.
 CC -----
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 CC -----
 DR EMBL: AL935258; CAD64544.1; --
 DR HSSP: P14900; 20AG.
 DR HAMAP: MF_00639; -; 1.
 DR InterPro: IPR004101; Mur_ligase_C.
 DR InterPro: IPR000713; Mur_ligase_N.
 DR InterPro: IPR005762; MurD.

DR Pfam; PF01225; Mur Ligase; 1.
 DR Pfam; PF02875; Mur Ligase C; 1.
 KW ATP-binding; Cell Division; Cell wall; Complete proteome; Ligase;
 KW Peptidoglycan synthesis.
 FT NE_BIND 119 125 ATP (Potential).
 SQ SEQUENCE 459 AA; 50137 MW; 083AB3E45C59DC9 CRC64;
 Query Match 13.3%; Score 6; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCERT 9
 DB 403 TDNCERT 408

RESULT 7
 ID Q9C7H2 PRELIMINARY; PRT; 601 AA.
 AC Q9C7H2;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Hypothetical protein F28P5.4 (A1972090/F28P5_4).
 GN Name=F28P5.4;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Roming C.M., Koo H., Fujii C.Y., Ulteback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nieman W.C., Fraser C.M.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bowser L., Carrinci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carrinci P.,
 RA Chan M.W., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Ondaera C.S.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC069273; AAG51137.1; -
 DR EMBL; AF367274; AAK56263.1; -
 DR EMBL; BT002712; AAO11628.1; -
 DR PIR; B96744; B96744.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR InterPro; IPR006638; E1p3/MiAb/MiB.
 DR InterPro; IPR007197; Radical_1ike_B.
 DR InterPro; IPR002792; Radical_SAM.
 DR InterPro; IPR005839; UPR0004.
 DR Pfam; PF04055; Radical_SAM; 1.
 DR Pfam; PF01938; TRAM; 1.
 DR Pfam; PF00919; UPR0004; 1.
 DR SMART; SM00729; E1p3; 1.
 DR TIGRFAMs; TIGR01578; MiAb-like-B; 1.
 DR TIGRFAMs; TIGR00089; UPR0004; 1.

DR PROSITE; PSS0926; TRAM; 1.
 DR PROSITE; PS01278; UPR0004; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 601 AA; 65496 MW; AAC13F7EFCED3DA3D CRC64;
 Query Match 13.3%; Score 6; DB 2; Length 601;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CERTC 12
 DB 514 CERTC 519

RESULT 8
 ID PRTS_SERMA STANDARD; PRT; 1045 AA.
 AC P09489;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Extracellular serine protease precursor (EC 3.4.21.-).
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OC NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-35 AND 407-408.
 RC STRAIN=IFO 3046;
 RX MEDLINE=86223815; PubMed=3011754;
 RA Yanagida N., Uozumi T., Beppu T.;
 RT "Specific excretion of Serratia marcescens protease through the outer
 RT membrane of Escherichia coli";
 RL J. Bacteriol. 166:937-944(1986).
 RN [2]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=92348352; PubMed=1639760;
 RA Shikata S., Shimada K., Kataoka H., Hornouchi S., Beppu T.;
 RT "Detection of large COOH-terminal domains processed from the precursor
 RT of Serratia marcescens serine protease in the outer membrane of
 RL Escherichia coli";
 RL J. Biochem. 111:627-632(1992).
 CC CC -1- SUBCELLULAR LOCATION: Secreted.
 CC CC -1- SIMILARITY: Belongs to the peptidase S8 family.
 CC CC
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 CC
 DR EMBL; M13469; AAA26572.1; -
 DR PIR; A29840; A29840.
 DR HSSP; Q99405; IMPT.
 DR MEROPS; S08.094; -
 DR InterPro; IPR005546; Auto.transpheta.
 DR InterPro; IPR006315; Autotransporter.
 DR InterPro; IPR000209; Pept_S8_S53.
 DR InterPro; IPR011165; Pept_S8A_autrans.
 DR Pfam; PF03797; Autotransporter; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PIRSF; PIRSF001164; Autotr_sbt_1ike; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR TIGRFAMs; TIGR01414; autotrans_part; 1.
 DR PROSITE; PS00136; SUBTILASE_ASP; FALSE_NEG.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Direct protein sequencing; Hydrolase; Serine protease; Signal;
 KW Zymogen.
 FT SIGNAL 1 27
 CHAIN 28 645 Extracellular serine protease.


```

FT PROPER 646 1045
FT ACT_SITE 76 76 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 341 341 Charge relay system (By similarity).
SQ SEQUENCE 1045 AA; 112345 MW; 4924EA50E4FF179C CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 1045;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 TEMQTD 20
Db 953 TEMQTD 958

RESULT 9
Q8IA76 PRELIMINARY; PRT; 1068 AA.
ID Q8IA76
AC Q8IA76;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform b.
GN Name=P11-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;
OC Rhabditidae; Peloderrinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Worldman P., Beck C.;
RT "The sequence of C. elegans cosmid K10F12.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 C2 domain.
EMBL; AF025462; AAN72423.1; -.
DR HSSP; P10688; 1DJH.
DR WormBase; WBGene00004045; p11-1.
DR WormPep; K10F12.3b; CE31037.
DR GO; GO:0004435; P:phospholipase C activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CalB.
DR InterPro; IPR001849; PH.

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DR InterPro; IPR011036; PH related.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_X.
DR InterPro; IPR01711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00148; PLCX; 1.
DR SMART; SM00149; PLCY; 1.
DR PROSITE; PSS0004; C2 DOMAIN 2; 1.
DR PROSITE; PSS0007; PI_PLC_X DOMAIN; 1.
DR PROSITE; PSS0008; PI_PLC_Y DOMAIN; 1.
SQ SEQUENCE 1068 AA; 12042 MW; 98F7CFCFFD7EC221 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 2; Length 1068;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TDNCET 9
Db 310 TDNCET 315

RESULT 10
Q8IA75 PRELIMINARY; PRT; 1075 AA.
ID Q8IA75
AC Q8IA75;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform a.
GN Name=P11-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditicoidea;
OC Rhabditidae; Peloderrinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Worldman P., Beck C.;
RT "The sequence of C. elegans cosmid K10F12.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

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Query Match 13.3%; Score 6; DB 2; Length 1870;
 Best Local Similarity 100.0%; Pred. No. 2e-02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
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 Db 241 NCERTCT 246

RESULT 14
 LMA2 HUMAN STANDARD; PRT, 3110 AA.
 AC P24043; Q14736; Q93022;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Laminin alpha-2 chain precursor (Laminin M chain) (Merotin heavy chain).
 GN Name=LMA2; Synonyms=LAMM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94124633; PubMed=8294519; DOI=10.1083/jcb.124.3.381;
 RA Violetteh R., Nissinen M., Sainio K., Byers M., Eddy R.,
 RA Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;
 RT "Human laminin M chain (merotin): complete primary structure,
 RT chromosomal assignment, and expression of the M and A chain in human
 RT fetal tissues.";
 RL J. Cell Biol. 124:381-394(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97066955; PubMed=8910357; DOI=10.1074/jbc.271.44.27664;
 RA Zhang X., Violetteh R., Tryggvason K.;
 RT "Structure of the human laminin alpha2-chain gene (LMA2), which is
 RT affected in congenital muscular dystrophy.";
 RL J. Biol. Chem. 271:27664-27669(1996).
 RN [3]
 RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90238994; PubMed=2185464;
 RA Ehrig K., Lelivo I., Agraves W.S., Ruoslahti E., Engvall E.;
 RT "Merotin, a tissue-specific basement membrane protein, is a laminin-
 RT like protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
 RN [4]
 RP VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluft G.A., Amato A.A., Mendell J.R.;
 RT "Novel single base polymorphisms and rare sequence variants in the
 RT laminin 2-chain coding region detected by RNA/SSC analysis.";
 RL Hum. Mutat. 13:174-174(1999).
 RN [5]
 RP ERRATUM.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluft G.A., Amato A.A., Mendell J.R.;
 RL Hum. Mutat. 13:340-340(1999).
 RN [6]
 RP VARIANT MDCA PRO-2564.
 RX MEDLINE=21476011; PubMed=11591856;
 RA He Y., Jones K.J., Vignier N., Morgan G., Chevallay M., Barois A.,
 RA Bessonnet-Machaud B., Hori H., Mizuta T., Tome F.M.S., North K.N.,
 RA Gutcheney P.;
 RT "Congenital muscular dystrophy with primary partial laminin alpha-2
 RT chain deficiency: molecular study.";
 RL Neurology 57:1319-1322(2001).
 RN [7]
 RP VARIANTS MDCA TYR-527 AND ARG-862.
 RX MEDLINE=22439669; PubMed=12552556; DOI=10.1002/humu.10157;

RA Terak Z., Prandini P., Boscaro M., Marin A., Devaney J., Marino M.,
 RA Fanin M., Trevisan C.P., Park J., Tyson W., Finkel R., Garcia C.,
 RA Angelini C., Hoffman E.P., Pegoraro E.;
 RT "Clinical and molecular study in congenital muscular dystrophy with
 RT partial laminin alpha-2 (LMA2) deficiency.";
 RL Hum. Mutat. 21:103-111(2003).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-2 chain is a subunit of laminin-2 (merotin) and
 CC laminin-4 (S-merotin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve,
 CC cardiac muscle, pancreas, lung, spleen, kidney, adrenal gland,
 CC skin, testis, meninges, choroid plexus, and some other regions of
 CC the brain; not in liver, thymus and bone.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domains VI, IV and G are globular.
 CC -1- DISEASE: Defects in LMA2 are the cause of merotin-deficient
 CC congenital muscular dystrophy type IA (MDCA) (MIM:607855). MDCA
 CC is characterized by difficulty walking, hypotonia, proximal
 CC weakness, hyporeflexia, and white matter hypodensity on MRI.
 CC -1- SIMILARITY: Contains 17 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 2 laminin IV domains.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -----
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 CC -----
 DR EMBL; Z26653; CAA81394.1; -;
 DR EMBL; U66796; AAB18388.1; JOINED.
 DR EMBL; U66733; AAB18388.1; JOINED.
 DR EMBL; U66734; AAB18388.1; JOINED.
 DR EMBL; U66735; AAB18388.1; JOINED.
 DR EMBL; U66736; AAB18388.1; JOINED.
 DR EMBL; U66737; AAB18388.1; JOINED.
 DR EMBL; U66738; AAB18388.1; JOINED.
 DR EMBL; U66739; AAB18388.1; JOINED.
 DR EMBL; U66740; AAB18388.1; JOINED.
 DR EMBL; U66741; AAB18388.1; JOINED.
 DR EMBL; U66742; AAB18388.1; JOINED.
 DR EMBL; U66743; AAB18388.1; JOINED.
 DR EMBL; U66744; AAB18388.1; JOINED.
 DR EMBL; U66745; AAB18388.1; JOINED.
 DR EMBL; U66746; AAB18388.1; JOINED.
 DR EMBL; U66747; AAB18388.1; JOINED.
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 DR EMBL; U66750; AAB18388.1; JOINED.
 DR EMBL; U66751; AAB18388.1; JOINED.
 DR EMBL; U66752; AAB18388.1; JOINED.
 DR EMBL; U66753; AAB18388.1; JOINED.
 DR EMBL; U66754; AAB18388.1; JOINED.
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 DR EMBL; U66756; AAB18388.1; JOINED.
 DR EMBL; U66757; AAB18388.1; JOINED.
 DR EMBL; U66758; AAB18388.1; JOINED.
 DR EMBL; U66759; AAB18388.1; JOINED.
 DR EMBL; U66760; AAB18388.1; JOINED.
 DR EMBL; U66761; AAB18388.1; JOINED.
 DR EMBL; U66762; AAB18388.1; JOINED.

DR EMBL: U66763; AAB18388.1; JOINED.
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 DR EMBL: U66767; AAB18388.1; JOINED.
 DR EMBL: U66768; AAB18388.1; JOINED.
 DR EMBL: U66769; AAB18388.1; JOINED.
 DR EMBL: U66770; AAB18388.1; JOINED.
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 DR EMBL: U66774; AAB18388.1; JOINED.
 DR EMBL: U66775; AAB18388.1; JOINED.
 DR EMBL: U66776; AAB18388.1; JOINED.
 DR EMBL: U66777; AAB18388.1; JOINED.
 DR EMBL: U66778; AAB18388.1; JOINED.
 DR EMBL: U66779; AAB18388.1; JOINED.
 DR EMBL: U66780; AAB18388.1; JOINED.
 DR EMBL: U66781; AAB18388.1; JOINED.
 DR EMBL: U66782; AAB18388.1; JOINED.
 DR EMBL: U66783; AAB18388.1; JOINED.
 DR EMBL: U66784; AAB18388.1; JOINED.
 DR EMBL: U66785; AAB18388.1; JOINED.
 DR EMBL: U66786; AAB18388.1; JOINED.
 DR EMBL: U66787; AAB18388.1; JOINED.
 DR EMBL: U66788; AAB18388.1; JOINED.
 DR EMBL: U66789; AAB18388.1; JOINED.
 DR EMBL: U66790; AAB18388.1; JOINED.
 DR EMBL: U66791; AAB18388.1; JOINED.
 DR EMBL: U66792; AAB18388.1; JOINED.
 DR EMBL: U66793; AAB18388.1; JOINED.
 DR EMBL: U66794; AAB18388.1; JOINED.
 DR EMBL: U66795; AAB18388.1; JOINED.
 DR EMBL: M59832; AAA63215.1; -.
 DR PIR: PX0082; MMHMH.
 DR HSSP: Q60675; 1DYK.
 DR GeneW: HGNC:6482; LAMA2.
 DR MIM: 156225; -.
 DR GO: GO:0005604; C:basement membrane; TAS.
 DR GO: GO:0005198; F:structural molecule activity; TAS.
 DR GO: GO:0007517; P:muscle development; TAS.
 DR InterPro: IPR008985; ConA_like_rec_91.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR008979; Gal_bind_like.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR000034; Laminin_B.
 DR InterPro: IPR002049; Laminin_BGF.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR009254; Laminin_I.
 DR InterPro: IPR010307; Laminin_II.
 DR InterPro: IPR008211; Laminin_N.
 DR InterPro: IPR003129; TSP_N.
 DR Pfam: PF00052; Laminin_B_2.
 DR Pfam: PF00053; Laminin_BGF_14.
 DR Pfam: PF00054; Laminin_G_5.
 DR Pfam: PF06008; Laminin_I_1.
 DR Pfam: PF06009; Laminin_II_1.
 DR Pfam: PF00055; Laminin_N_1.
 DR PRINTS: PR00011; EGFLAMININ.
 DR ProDom: PD003031; Laminin_B_2.
 DR PROSITE: PS00022; EGF_1; 11.
 DR PROSITE: PS01186; EGF_2; 3.
 DR PROSITE: PS00025; LAM_G_DOMAIN; 5.
 DR PROSITE: PS01248; LAMININ_TYPE_EGF_14.
 KW Basement membrane; Cell adhesion; Coiled coil;
 KW Congenital muscular dystrophy; Direct protein sequencing;

Query Match 13.3%; Score 6; DB 1; Length 3110;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
 |||||

DB 389 NCETCT 394

RESULT 15
 ID DEFA ANDAU STANDARD; PRT; 37 AA.
 AC P566E6; P81618; (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 4 kDa defensin.
 OS Androctonus australis (Sahara scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butirida; Butiridae; Butiridae; Androctonus.
 OC NCBI_TaxID=6858;
 RN (1)
 RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC STRAIN=Hector; TISSUE=Hemolymph;
 RX MEDLINE=97094646; PubMed=8939880; DOI=10.1074/jbc.271.47.29537;
 RA Ehret-Sabatier L., Loew D., Goyffon M., Fehlbauer F., Hoffmann J.A.,
 RA Van Dorsselaer A., Bulle P.;
 RT "Characterization of novel cysteine-rich antimicrobial peptides from
 scorpion blood.";
 RL J. Biol. Chem. 271:29537-29544(1996).
 CC -1- FUNCTION: Active against Gram-positive bacteria.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=4206.8; METHOD=Electrospray; RANGE=1-37;
 CC (1)
 CC NOTE=Ref.1.
 CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
 DR HSSP: P80571; 1FQN.
 DR InterPro: IPR001542; Defensin_2; 1.
 DR Pfam: PF01097; Defensin_2; 1.
 DR PROSITE: PS00425; ARTHROPOD_DEFENSINS; 1.
 KW Antibiotic; Defensin; Direct protein sequencing.
 FT DISULFID 4 25 By similarity.
 FT DISULFID 11 33 By similarity.
 FT DISULFID 15 35 By similarity.
 SQ SEQUENCE 37 AA; 4212 MW; AB1363BCE3FB84C1 CRC64;

Query Match 11.1%; Score 5; DB 1; Length 37;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 TCTCY 13
 |||||
 DB 32 TCTCT 36

Search completed: May 4, 2005, 14:33:21
 Job time : 82.2364 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:03:32 ; Search time 121.309 Seconds
(without alignments)
191.293 Million cell updates/sec

Title: US-09-977-406A-92

Perfect score: 60

Sequence: 1 EMQTDNCETCTCYETEMQTD.....TCYETEMQTDNCETCTCYET 60

Scoring table: OLIGO

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	96.7	60	5	AAO17999 Human PSP
2	45	75.0	45	5	AAO17998 Human PSP
3	30	50.0	30	5	AAO17997 Human PSP
4	16	26.7	16	5	AAO17917 Human pro
5	16	26.7	17	5	AAO17918 Human pro
6	16	26.7	18	5	AAO17919 Human pro
7	16	26.7	19	5	AAO17920 Human pro
8	16	26.7	20	5	AAO17921 Human pro
9	16	26.7	21	5	AAO17922 Human pro
10	16	26.7	22	5	AAO17923 Human pro
11	16	26.7	23	5	AAO17924 Human pro
12	16	26.7	24	5	AAO17925 Human pro
13	16	26.7	25	5	AAO17926 Human pro
14	16	26.7	26	5	AAO17927 Human pro
15	16	26.7	27	5	AAO17928 Human pro
16	16	26.7	28	5	AAO17929 Human pro
17	16	26.7	29	5	AAO17930 Human pro
18	16	26.7	30	5	AAO17931 Human pro
19	16	26.7	31	5	AAO17932 Human pro
20	16	26.7	32	5	AAO17933 Human pro
21	16	26.7	33	5	AAO17934 Human pro
22	16	26.7	34	5	AAO17935 Human pro
23	16	26.7	35	5	AAO17936 Human pro
24	16	26.7	36	5	AAO17937 Human pro
25	16	26.7	37	5	AAO17938 Human pro

ALIGNMENTS

RESULT 1	
ID AAO17999	standard; protein; 60 AA.
XX	
AC AAO17999;	
XX	
DT 30-AUG-2002	(first entry)
XX	
DE Human PSP94 analogue adaptor peptide #3.	
XX	
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;	
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;	
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;	
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;	
KW benign prostate hyperplasia; cytostatic.	
XX	
OS Synthetic.	
XX	
PN WO200233090-A2.	
XX	
PD 25-APR-2002.	
XX	
PF 15-OCT-2001; 2001MO-CA001463.	
XX	
PR 16-OCT-2000; 2000CA-02321256.	
PR 20-AUG-2001; 2001CA-0235534.	
XX	
PA (PRO-) PROCYON BIOPHARMA INC.	
XX	
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;	
XX	
DR WPI; 2002-471401/50.	
XX	
PT New human prostate secretory protein of 94 amino acids, useful for	
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,	
PT gastrointestinal, breast, endometrial, and ovarian cancers.	
XX	
PS Disclosure; Page 106; 185pp; English.	
XX	
CC The present invention relates to analogues of the human prostate	
CC secretory protein of 94 amino acids (PSP94, also known as prostatic	
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-	
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting	
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal	
CC cancer, breast cancer, endometrial, ovarian or other cancers of	
CC epithelial secretion, or benign prostate hyperplasia and for treating	
CC patients with a disease characterized by elevated levels of PSH. The	
CC present sequence is an adaptor peptide useful in the invention	

XX
SQ Sequence 60 AA;

Query Match 96.7%; Score 58; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 8.6e-58;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCECTCTCYETEMQTDNCECTCTCYETEMQTDNCECTCTCYET 58
DB 1 EMQTDNCECTCTCYETEMQTDNCECTCTCYETEMQTDNCECTCTCYET 58

RESULT 2
AA017998
ID AA017998 standard; protein; 45 AA.

XX
AC AA017998;

XX
DT 30-AUG-2002 (first entry)

XX
DE Human PSP94 analogue adaptor peptide #2.

XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.

XX
OS Synthetic.

XX
PN W0200233090-A2.

XX
PD 25-APR-2002.

XX
PF 15-OCT-2001; 2001WO-CA001463.

XX
PR 16-OCT-2000; 2000CA-02321256.
20-AUG-2001; 2001CA-02355334.

XX
PA (PROC-) PROCYON BIOPHARMA INC.

XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

XX
DR WPI, 2002-471401/50.

XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX
PS Disclosure; Page 106; 185pp; English.

XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an adaptor peptide useful in the invention

XX
SQ Sequence 45 AA;

Query Match 75.0%; Score 45; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCECTCTCYETEMQTDNCECTCTCYETEMQTDNCECTCTCYET 45
DB 1 EMQTDNCECTCTCYETEMQTDNCECTCTCYETEMQTDNCECTCTCYET 45

RESULT 3

AA017997
ID AA017997 standard; peptide; 30 AA.

XX
AC AA017997;

XX
DT 30-AUG-2002 (first entry)

XX
DE Human PSP94 analogue adaptor peptide #1.

XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.

XX
OS Synthetic.

XX
PN W0200233090-A2.

XX
PD 25-APR-2002.

XX
PF 15-OCT-2001; 2001WO-CA001463.

XX
PR 16-OCT-2000; 2000CA-02321256.
20-AUG-2001; 2001CA-02355334.

XX
PA (PROC-) PROCYON BIOPHARMA INC.

XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

XX
DR WPI, 2002-471401/50.

XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX
PS Disclosure; Page 105; 185pp; English.

XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostate hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an adaptor peptide useful in the invention

XX
SQ Sequence 30 AA;

Query Match 50.0%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQTDNCECTCTCYETEMQTDNCECTCTCYET 30
DB 1 EMQTDNCECTCTCYETEMQTDNCECTCTCYET 30

RESULT 4
AA017917
ID AA017917 standard; peptide; 16 AA.

XX
AC AA017917;

XX
DT 30-AUG-2002 (first entry)

XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #6.

XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

PA	(PROC-)PROCYON BIOPHARMA INC.
XX	
PI	Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
DR	WPI; 2002-471401/50.
XX	
PT	New human prostate secretory protein of 94 amino acids, useful for
PT	inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT	gastrointestinal, breast, endometrial, and ovarian cancers.
PS	Claim 2; Page 76; 185pp; English.
XX	
CC	The present invention relates to analogues of the human prostate
CC	secretory protein of 94 amino acids (PSP94, also known as prostatic
CC	inhibin peptide (PI), human seminal plasma inhibin (HSPi) and beta-
CC	microseminoprotein (beta-MSP). The analogues are useful for inhibiting
CC	growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC	cancer, breast cancer, endometrial, ovarian or other cancers of
CC	epithelial secretion, or benign prostatic hyperplasia and for treating
CC	patients with a disease characterized by elevated levels of FSH. The
CC	present sequence is an analogue of the invention
SQ	
	Sequence 17 AA;
Query Match	26.7%; Score 16; DB 5; Length 17;
Best Local Similarity	100.0%; Pred. No. 3.2e-11;
Matches 16; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 EWQTNCECTCYETE 16
Db	1 EWQTNCECTCYETE 16
RESULT 6	
AA017919	
ID	AA017919 standard; peptide: 18 AA.
XX	
AC	AA017919;
XX	
DT	30-AUG-2002 (first entry)
XX	
DE	Human prostate secretory protein of 94 amino acids PSP94 analogue #8.
XX	
KW	Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
KW	beta-microseminoprotein; human seminal plasma inhibin; analogue;
KW	prostatic secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW	stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW	benign prostate hyperplasia; cyrostatic.
XX	
XX	
OS	Homo sapiens.
XX	
PN	WO200233090-A2.
XX	
PD	25-APR-2002.
XX	
PF	15-OCT-2001; 2001WO-CA001463.
XX	
PR	16-OCT-2000; 2000CA-02321256.
XX	
FR	20-AUG-2001; 2001CA-02355334.
XX	
PA	(PROC-) PROCYON BIOPHARMA INC.
XX	
PI	Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;
XX	
DR	WPI; 2002-471401/50.
XX	
PT	New human prostate secretory protein of 94 amino acids, useful for
PT	inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT	gastrointestinal, breast, endometrial, and ovarian cancers.
XX	
XX	Claim 2; Page 77; 185pp; English.
XX	
CC	The present invention relates to analogues of the human prostate

CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemnoprotein (beets-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 18 AA;
Query Match 26.7%; Score 16; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQTDNCECTCYETE 16
DB 1 EMQTDNCECTCYETE 16
RESULT 7
AAOI7920
ID AAOI7920 standard; peptide; 19 AA.
XX
AC AAOI7920;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #9.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
KW beta-microsemnoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200233090-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
DR WPI; 2002-471401/50.
XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 77; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemnoprotein (beets-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 19 AA;
Query Match 26.7%; Score 16; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQTDNCECTCYETE 16
DB 1 EMQTDNCECTCYETE 16
RESULT 8
AAOI7921
ID AAOI7921 standard; peptide; 20 AA.
XX
AC AAOI7921;
XX
DT 30-AUG-2002 (first entry)
XX
DE Human prostate secretory protein of 94 amino acids PSP94 analogue #10.
XX
KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
KW beta-microsemnoprotein; human seminal plasma inhibin; analogue;
KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
KW benign prostate hyperplasia; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200233090-A2.
XX
PD 25-APR-2002.
XX
PF 15-OCT-2001; 2001WO-CA001463.
XX
PR 16-OCT-2000; 2000CA-02321256.
XX
PR 20-AUG-2001; 2001CA-02355334.
XX
PA (PROC-) PROCYON BIOPHARMA INC.
XX
PI Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;
XX
DR WPI; 2002-471401/50.
XX
PT New human prostate secretory protein of 94 amino acids, useful for
PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
PT gastrointestinal, breast, endometrial, and ovarian cancers.
XX
PS Claim 2; Page 77; 185pp; English.
XX
CC The present invention relates to analogues of the human prostate
CC secretory protein of 94 amino acids (PSP94, also known as prostatic
CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
CC microsemnoprotein (beets-MSP)). The analogues are useful for inhibiting
CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
CC cancer, breast cancer, endometrial, ovarian or other cancers of
CC epithelial secretion, or benign prostatic hyperplasia and for treating
CC patients with a disease characterized by elevated levels of FSH. The
CC present sequence is an analogue of the invention
XX
SQ Sequence 20 AA;
Query Match 26.7%; Score 16; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EMQTDNCECTCYETE 16
DB 1 EMQTDNCECTCYETE 16
RESULT 9
AAOI7922
ID AAOI7922 standard; peptide; 21 AA.
XX
AC AAOI7922;
XX

DT 30-AUG-2002 (first entry)
 XX
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #11.
 XX
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200233090-A2.
 XX
 XX 25-APR-2002.
 XX
 PD 15-OCT-2001; 2001WO-CA001463.
 XX
 PF 16-OCT-2000; 2000CA-02321256.
 XX
 PR 20-AUG-2001; 2001CA-02355334.
 XX
 PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 PI Garde S, Panchal CU, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX
 DR WPI; 2002-471401/50.
 XX
 XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX
 PS Claim 2; Page 78; 185pp; English.
 XX
 CC The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 CC
 SQ Sequence 21 AA;
 XX
 Query Match 26.7%; Score 16; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.8e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMQTDNCTCTCYETE 16
 DB 1 EMQTDNCTCTCYETE 16
 XX
 RESULT 10
 AA017923
 ID AA017923 standard; peptide; 22 AA.
 XX
 AC AA017923;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #12.
 XX
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200233090-A2.
 XX

XX
 PD 25-APR-2002.
 XX
 PF 15-OCT-2001; 2001WO-CA001463.
 XX
 PR 16-OCT-2000; 2000CA-02321256.
 XX
 PR 20-AUG-2001; 2001CA-02355334.
 XX
 PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 PI Garde S, Panchal CU, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX
 DR WPI; 2002-471401/50.
 XX
 XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.
 XX
 PS Claim 2; Page 78; 185pp; English.
 XX
 CC The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-
 CC microseminoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention
 CC
 SQ Sequence 22 AA;
 XX
 Query Match 26.7%; Score 16; DB 5; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMQTDNCTCTCYETE 16
 DB 1 EMQTDNCTCTCYETE 16
 XX
 RESULT 11
 AA017924
 ID AA017924 standard; peptide; 23 AA.
 XX
 AC AA017924;
 XX
 DT 30-AUG-2002 (first entry)
 XX
 DE Human prostate secretory protein of 94 amino acids PSP94 analogue #13.
 XX
 KW Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;
 KW beta-microseminoprotein; human seminal plasma inhibin; analogue;
 KW prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KW stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KW benign prostate hyperplasia; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200233090-A2.
 XX
 XX 25-APR-2002.
 XX
 PD 15-OCT-2001; 2001WO-CA001463.
 XX
 PF 16-OCT-2000; 2000CA-02321256.
 XX
 PR 20-AUG-2001; 2001CA-02355334.
 XX
 PA (PROC-) PROCYON BIOPHARMA INC.
 XX
 PI Garde S, Panchal CU, Bajjal-Gupta M, Fraser J, Kadhim S;
 XX
 DR WPI; 2002-471401/50.
 XX

XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 78; 185pp; English.

XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microsemionoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention

XX Sequence 23 AA;

Query Match 26.7%; Score 16; DB 5; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4,1e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQDNCETCTCYETE 16
 |||||
 Db 1 EMQDNCETCTCYETE 16

RESULT 12

AAOI7925
 ID AAO17925 standard; peptide; 24 AA.

XX AAO17925;

DT 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #14.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KM beta-microsemionoprotein; human seminal plasma inhibin; analogue;
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

OS WO200233090-A2.

PN 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

PR 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC;

PA Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

PI WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 78; 185pp; English.

XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microsemionoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of

CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention

XX Sequence 24 AA;

Query Match 26.7%; Score 16; DB 5; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4,3e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQDNCETCTCYETE 16
 |||||
 Db 1 EMQDNCETCTCYETE 16

RESULT 13

AAOI7926
 ID AAO17926 standard; peptide; 25 AA.

XX AAO17926;

DT 30-AUG-2002 (first entry)

XX Human prostate secretory protein of 94 amino acids PSP94 analogue #15.

XX Cancer; human; PSP94; prostatic inhibin protein; PIP; HSPi; beta-MSP;
 KM beta-microsemionoprotein; human seminal plasma inhibin; analogue;
 KM prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;
 KM stomach cancer; breast cancer; endometrial cancer; ovarian cancer;
 KM benign prostate hyperplasia; cytostatic.

XX Homo sapiens.

OS WO200233090-A2.

PN 25-APR-2002.

XX 15-OCT-2001; 2001WO-CA001463.

XX 16-OCT-2000; 2000CA-02321256.

PR 20-AUG-2001; 2001CA-02355334.

XX (PROC-) PROCYON BIOPHARMA INC.

PA Garde S, Panchal CJ, Baijal-Gupta M, Fraser J, Kadhim S;

PI WPI; 2002-471401/50.

XX New human prostate secretory protein of 94 amino acids, useful for
 PT inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,
 PT gastrointestinal, breast, endometrial, and ovarian cancers.

XX Claim 2; Page 79; 185pp; English.

XX The present invention relates to analogues of the human prostate
 CC secretory protein of 94 amino acids (PSP94, also known as prostatic
 CC inhibin peptide (PIP), human seminal plasma inhibin (HSPi) and beta-
 CC microsemionoprotein (beta-MSP)). The analogues are useful for inhibiting
 CC growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal
 CC cancer, breast cancer, endometrial, ovarian or other cancers of
 CC epithelial secretion, or benign prostate hyperplasia and for treating
 CC patients with a disease characterized by elevated levels of FSH. The
 CC present sequence is an analogue of the invention

XX Sequence 25 AA;

Query Match 26.7%; Score 16; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4,5e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EMQDNCETCTCYETE 16
 |||||
 Db 1 EMQDNCETCTCYETE 16

RESULT 14

AA017927

ID AA017927 standard; peptide, 26 AA.

AA017927;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94 analogue #16.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-microseminoprotein; human seminal plasma inhibin; analogue;

prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

benign prostate hyperplasia; cytostatic.

Homo sapiens.

MO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 79; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 26 AA;

Query Match 26.7%; Score 16; DB 5; Length 26;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EWQDNCETCTCYETE 16

1 EWQDNCETCTCYETE 16

AA017928 standard; peptide, 27 AA.

AA017928;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94 analogue #17.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

beta-microseminoprotein; human seminal plasma inhibin; analogue;

prostate secretory protein of 94 amino acids; prostatic adenocarcinoma;

stomach cancer; breast cancer; endometrial cancer; ovarian cancer;

benign prostate hyperplasia; cytostatic.

Homo sapiens.

MO200233090-A2.

25-APR-2002.

15-OCT-2001; 2001WO-CA001463.

16-OCT-2000; 2000CA-02321256.

20-AUG-2001; 2001CA-02355334.

(PROC-) PROCYON BIOPHARMA INC.

Garde S, Panchal CJ, Bajjal-Gupta M, Fraser J, Kadhim S;

WPI; 2002-471401/50.

New human prostate secretory protein of 94 amino acids, useful for

inhibiting growth of e.g. tumor, prostatic adenocarcinoma, stomach,

gastrointestinal, breast, endometrial, and ovarian cancers.

Claim 2; Page 79; 185pp; English.

The present invention relates to analogues of the human prostate

secretory protein of 94 amino acids (PSP94, also known as prostatic

inhibin peptide (PIP), human seminal plasma inhibin (HSP1) and beta-

microseminoprotein (beta-MSP). The analogues are useful for inhibiting

growth of tumours, prostatic adenocarcinoma, stomach or gastrointestinal

cancer, breast cancer, endometrial, ovarian or other cancers of

epithelial secretion, or benign prostate hyperplasia and for treating

patients with a disease characterized by elevated levels of FSH. The

present sequence is an analogue of the invention

Sequence 27 AA;

Query Match 26.7%; Score 16; DB 5; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.8e-11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EWQDNCETCTCYETE 16

1 EWQDNCETCTCYETE 16

AA017928 standard; peptide, 27 AA.

AA017928;

30-AUG-2002 (first entry)

Human prostate secretory protein of 94 amino acids PSP94 analogue #17.

Cancer; human; PSP94; prostatic inhibin protein; PIP; HSP1; beta-MSP;

Search completed: May 4, 2005, 14:25:12

Job time : 122.309 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:13:33 ; Search time 30.7636 Seconds
(without alignments)
145.592 Million cell updates/sec

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Perfect score: 60
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Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	26.7	94	US-07-899-535A-1	Sequence 1, Appl
2	16	26.7	114	US-09-513-999C-7807	Sequence 17, Appl
3	6	10.0	241	US-08-460-309-17	Sequence 17, Appl
4	6	10.0	241	US-08-125-077-17	Sequence 17, Appl
5	6	10.0	362	US-09-248-796A-20514	Sequence 20514, A
6	6	10.0	2123	US-09-949-016-7517	Sequence 7517, Ap
7	6	10.0	3070	US-09-961-403-7	Sequence 7, Appl
8	6	10.0	3089	US-09-562-702A-8	Sequence 8, Appl
9	6	10.0	3089	US-09-562-702A-4	Sequence 4, Appl
10	6	10.0	3110	US-09-562-702A-2	Sequence 2, Appl
11	6	10.0	3110	US-09-562-702A-6	Sequence 6, Appl
12	6	10.0	3110	US-09-561-709B-7	Sequence 86, Appl
13	6	10.0	3110	US-09-917-254-86	Sequence 86, Appl
14	6	10.0	3111	US-09-949-016-5937	Sequence 5937, Ap
15	6	10.0	3111	US-08-460-309-4	Sequence 4, Appl
16	5	10.0	3111	US-08-125-077-4	Sequence 4, Appl
17	5	8.3	9	US-08-481-968A-24	Sequence 24, Appl
18	5	8.3	9	US-08-154-712B-24	Sequence 24, Appl
19	5	8.3	9	US-09-947-925A-24	Sequence 24, Appl
20	5	8.3	37	US-09-917-340-57	Sequence 57, Appl
21	5	8.3	37	US-09-829-481-11	Sequence 11, Appl
22	5	8.3	38	US-09-030-619-199	Sequence 199, App
23	5	8.3	38	US-09-030-619-200	Sequence 200, App
24	5	8.3	58	US-09-621-976-5440	Sequence 5440, Ap
25	5	8.3	75	US-09-107-532A-4113	Sequence 4113, Ap
26	5	8.3	104	US-09-621-976-6750	Sequence 6750, Ap
27	5	8.3	107	US-09-513-999C-7986	Sequence 7986, Ap

28	5	8.3	110	US-09-513-999C-7055	Sequence 7055, Ap
29	5	8.3	188	US-09-270-767-61692	Sequence 61692, A
30	5	8.3	192	US-08-685-466C-4	Sequence 4, Appl
31	5	8.3	230	US-09-248-796A-21826	Sequence 21826, A
32	5	8.3	231	US-09-265-540E-4	Sequence 4, Appl
33	5	8.3	243	US-08-460-309-15	Sequence 15, Appl
34	5	8.3	243	US-08-460-309-16	Sequence 16, Appl
35	5	8.3	243	US-08-125-077-15	Sequence 15, Appl
36	5	8.3	243	US-08-125-077-16	Sequence 16, Appl
37	5	8.3	259	US-09-328-352-5038	Sequence 5038, Ap
38	5	8.3	261	US-09-962-357-8	Sequence 8, Appl
39	5	8.3	314	US-08-486-036A-4	Sequence 4, Appl
40	5	8.3	314	US-09-005-238-4	Sequence 4, Appl
41	5	8.3	314	US-08-768-619-4	Sequence 4, Appl
42	5	8.3	314	PCT-US96-09848-4	Sequence 4, Appl
43	5	8.3	315	US-09-902-540-14527	Sequence 14527, A
44	5	8.3	316	US-08-482-282B-4	Sequence 4, Appl
45	5	8.3	316	US-09-543-681A-5873	Sequence 5873, Ap

ALIGNMENTS

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RESULT 1
US-07-899-535A-1
; Sequence 1, Application US/07899535A
; Patent No. 5428011
; GENERAL INFORMATION:
; APPLICANT: Sheth, Anil R.
; APPLICANT: Garde, Seema
; TITLE OF INVENTION: Pharmaceutical Preparations For
; TITLE OF INVENTION: Inhibiting Tumours Associated With Prostate
; TITLE OF INVENTION: Adenocarcinoma, Stomach Cancer and Breast Cancer.
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Mr. George Loud
; STREET: 2001 Jefferson Davis Highway, Suite 306
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/899,535A
; FILING DATE: 16-JUN-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Loud, George A.
; REGISTRATION NUMBER: 25,814
; REFERENCE/DOCKET NUMBER: S&B-A835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-415-0960
; TELEFAX: 703-415-0962
; TELEX: 24 8614
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; US-07-899-535A-1
;
Query Match 26.7%; Score 16; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 7e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 EMQDNCETCTCYETE 16
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Db 31 EMQDNCETCTCYETE 46

RESULT 2

US-09-513-999C-7807
; Sequence 7807, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7807
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20...-1
; OTHER INFORMATION: score 9
; OTHER INFORMATION: seq VVIFATFVLICNA/SC
US-09-513-999C-7807

Query Match 26.7%; Score 16; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 8,4e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 EMQDNCETCTCYETE 16
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Db 51 EMQDNCETCTCYETE 66

RESULT 3

US-08-460-309-17
; Sequence 17, Application US/08460309
; Patent No. 5837496
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,309
; FILING DATE: 21-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,077
; FILING DATE: 22-SEP-1993
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/472,319
FILING DATE: 30-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/919,951
FILING DATE: 27-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9721
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-460-309-17

Query Match 10.0%; Score 6; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 NCETCT 11
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Db 103 NCETCT 108

RESULT 4

US-08-125-077-17
; Sequence 17, Application US/08125077
; Patent No. 5872231
; Patent No. 5872231 5840863
; GENERAL INFORMATION:
; APPLICANT: Engvall, Eva
; APPLICANT: Leivo, Ilmo
; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
; TITLE OF INVENTION: Fragments and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,077
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US 94/10730
; FILING DATE: 21-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/472,319
; FILING DATE: 30-JAN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/919,951
; FILING DATE: 27-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9721
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 17:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-125-077-17

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Query Match	10.0%;	Score 6;	DB 2;	Length 241;
Best Local Similarity	100.0%;	Pred. No. 7.9;		
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	6	NCETCT	11
Db	103	NCETCT	108

RESULT 5
US-09-248-796A-20514
Sequence 20514, Application US/09248796A
Patent No. 6747127

```

# APPLICANT: Kelch Weinstein et al
# TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
# TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
# FILE REFERENCE: 107196.132
# CURRENT APPLICATION NUMBER: US/09/248,796A
# CURRENT FILING DATE: 1998-02-12
# PRIOR APPLICATION NUMBER: US 60/074,725
# PRIOR FILING DATE: 1998-02-13
# PRIOR APPLICATION NUMBER: US 60/096,409
# PRIOR FILING DATE: 1998-08-13
# NUMBER OF SEQ ID NOS: 28208
# SEQ ID NO 20514
# LENGTH: 362
# TYPE: PRT
# ORGANISM: Candida albicans
# US-09-248-796A-20514

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Query Match	10.0%;	Score 6;	DB 4;	Length 362;
Best Local Similarity	100.0%;	Pred. No. 11;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	15	TEWQTD	20
Db	341	TEWQTD	346

RESULT 6
US-09-949-016-7517
; Sequence 7517, Application US/09949016

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1  APPLICANT: VENTER, J. Craig et al.
2  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
3  TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
4  FILE REFERENCE: CLO001307
5  CURRENT APPLICATION NUMBER: US/09/949,016
6  CURRENT FILING DATE: 2000-04-14
7  PRIOR APPLICATION NUMBER: 60/241,755
8  PRIOR FILING DATE: 2000-10-20
9  PRIOR APPLICATION NUMBER: 60/237,768
10 PRIOR FILING DATE: 2000-10-03
11 PRIOR APPLICATION NUMBER: 60/231,498
12 PRIOR FILING DATE: 2000-09-08
13 NUMBER OF SEQ ID NOS: 207012
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 7517
16 LENGTH: 2123
17 TYPE: prt
18 ORGANISM: Human
19 US-09-949-016-7517

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Query Match	10.0%;	Score 6;	DB 4;	Length 2123;
Best Local Similarity	100.0%;	Pred. No. 59;		

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Qy	6	NCERCCT	11			
Db	405	NCERCCT	410			

RESULT 7
US-09-961-403-7
; Sequence 7, Application US/09961403
; Patent No. 6780594

```

APPLICANT: HE-STUMP, HOLGER
APPLICANT: HAENDLER, BERNARD
APPLICANT: KRAETSCHMAR, JOERN
APPLICANT: KREFT, BERTHOLT
APPLICANT: WINTERHAGER, ELKE
APPLICANT: RECIDOR, PEDRO
APPLICANT: SCOTTI, SIMONE
TITLE OF INVENTION: METHOD FOR IN VITRO DIAGNOSIS OF ENDOMETRIOSIS
FILE REFERENCE: SCH-1789
CURRENT APPLICATION NUMBER: US/09/961,403
CURRENT FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 3070
TYPE: FRT
ORGANISM: Homo sapiens
US-09-961-403-7

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Query Match	10.0%;	Score 6;	DB 4;	Length 3070;
Best Local Similarity	100.0%;	Pred. No. 82;		
Matches	6;	Conservative	0;	Mismatches
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QY      6 NCETCT  11
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Db     389 NCETCT 394
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RESULT 8
US-09-562-702A-8
; Sequence 8, Application US/09562702A
; Patent No. 6632790

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1  APPLICANT: yurchenco, Peter
2  TITLE OF INVENTION: Laminin 2 and Methods for Its Use
3  FILE REFERENCE: 99-274-B
4  CURRENT APPLICATION NUMBER: US/09/562,702A
5  CURRENT FILING DATE: 2000-04-28
6  PRIOR APPLICATION NUMBER: 60/155,945
7  PRIOR FILING DATE: 1999-09-24
8  PRIOR APPLICATION NUMBER: 60/143,289
9  PRIOR FILING DATE: 1999-07-12
10 PRIOR APPLICATION NUMBER: 60/139,198
11 PRIOR FILING DATE: 1999-06-15
12 PRIOR APPLICATION NUMBER: 60/131,720
13 PRIOR FILING DATE: 1999-04-30
14 NUMBER OF SEQ ID NOS: 32
15 SOFTWARE: PatentIn Ver. 2.0
16 SEQ ID NO. 8
17 LENGTH: 3088
18 TYPE: PRT
19 ORGANISM: Homo sapiens
20 US-09-562-702A-8

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Query Match	10.0%;	Score 6;	DB 4;	Length 3088;
Best Local Similarity	100.0%;	Pred. No. 83;		
Matches	6;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY	6	NCETCT	11
Db	367	NCETCT	372

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RESULT 9
US-09-562-702A-4
; Sequence 4, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 3089
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-4
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Query Match
Best Local Similarity 10.0%; Score 6; DB 4; Length 3110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 NCERTCT 11
Db 367 NCERTCT 372
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RESULT 10
US-09-562-702A-2
; Sequence 2, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-2
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Query Match
Best Local Similarity 10.0%; Score 6; DB 4; Length 3110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 NCERTCT 11
Db 389 NCERTCT 394
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RESULT 11
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US-09-562-702A-6
; Sequence 6, Application US/09562702A
; Patent No. 6632790
; GENERAL INFORMATION:
; APPLICANT: Yurchenco, Peter
; TITLE OF INVENTION: Laminin 2 and Methods for Its Use
; FILE REFERENCE: 99-274-B
; CURRENT APPLICATION NUMBER: US/09/562,702A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/155,945
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 60/143,289
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/139,198
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/131,720
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-562-702A-6
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Query Match
Best Local Similarity 10.0%; Score 6; DB 4; Length 3110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 NCERTCT 11
Db 389 NCERTCT 394
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RESULT 12
US-09-561-709B-7
; Sequence 7, Application US/09561709B
; Patent No. 6682911
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Champliand, Marie-France
; APPLICANT: Olson, Pamela
; APPLICANT: Koch, Manuel
; APPLICANT: Bruken, William
; TITLE OF INVENTION: LAMININS AND USES THEREOF
; FILE REFERENCE: 10287-060001
; CURRENT APPLICATION NUMBER: US/09/561,709B
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 09/168,949
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 60/061,609
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-709B-7
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Query Match
Best Local Similarity 10.0%; Score 6; DB 4; Length 3110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 6 NCERTCT 11
Db 389 NCERTCT 394
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RESULT 13
US-09-917-254-86
; Sequence 86, Application US/09917254
; Patent No. 6703204
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/ GENERAL INFORMATION:
/ APPLICANT: Mutter, George
/ APPLICANT: Baak, Jan
/ TITLE OF INVENTION: Prognostic Classification of Breast Cancer
/ FILE REFERENCE: B0801/7224 (JRV)
/ CURRENT APPLICATION NUMBER: US/09/917,254
/ CURRENT FILING DATE: 2001-07-27
/ PRIOR APPLICATION NUMBER: US 60/222,093
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 86
/ LENGTH: 3110
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-917-254-86

Query Match          10.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 NCERTCT 11
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Db      389 NCERTCT 394

RESULT 14
US-09-949-016-5937
/ Sequence 5937, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5937
/ LENGTH: 3110
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-5937

Query Match          10.0%; Score 6; DB 4; Length 3110;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 NCERTCT 11
        |||||
Db      389 NCERTCT 394

RESULT 15
US-08-460-309-4
/ Sequence 4, Application US/08460309
/ Patent No. 5837496
/ GENERAL INFORMATION:
/ APPLICANT: Engvall, Eva
/ APPLICANT: Leivo, Ilmo
/ TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
/ TITLE OF INVENTION: Fragments and Uses Thereof
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Campbell and Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
```

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/ CITY: San Diego
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/460,309
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/125,077
/ FILING DATE: 22-SEP-1993
/ APPLICATION NUMBER: US PCT/US 94/10730
/ FILING DATE: 21-SEP-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/472,319
/ FILING DATE: 30-JAN-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/919,951
/ FILING DATE: 27-JUL-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-LA 9721
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3111 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
US-08-460-309-4

Query Match          10.0%; Score 6; DB 2; Length 3111;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 NCERTCT 11
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Db      389 NCERTCT 394

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Job time : 31.7636 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:33:36 / Search time 66.9818 Seconds
(without alignments)
298.385 Million cell updates/sec

Title: US-09-977-406A-92

Perfect score: 60
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Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1426032 seqs, 333106140 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database: Published Applications AA:

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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	60	US-09-977-406A-92	Sequence 92, Appl
2	45	75.0	45	US-09-977-406A-91	Sequence 91, Appl
3	30	50.0	30	US-09-977-406A-90	Sequence 90, Appl
4	16	26.7	16	US-09-977-406A-10	Sequence 10, Appl
5	16	26.7	17	US-09-977-406A-11	Sequence 11, Appl
6	16	26.7	18	US-09-977-406A-12	Sequence 12, Appl
7	16	26.7	19	US-09-977-406A-13	Sequence 13, Appl
8	16	26.7	20	US-09-977-406A-14	Sequence 14, Appl
9	16	26.7	21	US-09-977-406A-15	Sequence 15, Appl
10	16	26.7	22	US-09-977-406A-16	Sequence 16, Appl
11	16	26.7	23	US-09-977-406A-17	Sequence 17, Appl
12	16	26.7	24	US-09-977-406A-18	Sequence 18, Appl
13	16	26.7	25	US-09-977-406A-19	Sequence 19, Appl

14	16	26.7	26	10	US-09-977-406A-20	Sequence 20, Appl
15	16	26.7	27	10	US-09-977-406A-21	Sequence 21, Appl
16	16	26.7	28	10	US-09-977-406A-22	Sequence 22, Appl
17	16	26.7	29	10	US-09-977-406A-23	Sequence 23, Appl
18	16	26.7	30	10	US-09-977-406A-24	Sequence 24, Appl
19	16	26.7	31	10	US-09-977-406A-25	Sequence 25, Appl
20	16	26.7	32	10	US-09-977-406A-26	Sequence 26, Appl
21	16	26.7	33	10	US-09-977-406A-27	Sequence 27, Appl
22	16	26.7	34	10	US-09-977-406A-28	Sequence 28, Appl
23	16	26.7	35	10	US-09-977-406A-29	Sequence 29, Appl
24	16	26.7	36	10	US-09-977-406A-30	Sequence 30, Appl
25	16	26.7	37	10	US-09-977-406A-31	Sequence 31, Appl
26	16	26.7	38	10	US-09-977-406A-32	Sequence 32, Appl
27	16	26.7	39	10	US-09-977-406A-33	Sequence 33, Appl
28	16	26.7	40	10	US-09-977-406A-34	Sequence 34, Appl
29	16	26.7	41	10	US-09-977-406A-35	Sequence 35, Appl
30	16	26.7	42	10	US-09-977-406A-36	Sequence 36, Appl
31	16	26.7	43	10	US-09-977-406A-37	Sequence 37, Appl
32	16	26.7	44	10	US-09-977-406A-38	Sequence 38, Appl
33	16	26.7	45	10	US-09-977-406A-39	Sequence 39, Appl
34	16	26.7	46	10	US-09-977-406A-40	Sequence 40, Appl
35	16	26.7	47	10	US-09-977-406A-41	Sequence 41, Appl
36	16	26.7	48	10	US-09-977-406A-42	Sequence 42, Appl
37	16	26.7	49	10	US-09-977-406A-43	Sequence 43, Appl
38	16	26.7	50	10	US-09-977-406A-44	Sequence 44, Appl
39	16	26.7	51	10	US-09-977-406A-45	Sequence 45, Appl
40	16	26.7	52	10	US-09-977-406A-46	Sequence 46, Appl
41	16	26.7	53	10	US-09-977-406A-47	Sequence 47, Appl
42	16	26.7	54	10	US-09-977-406A-48	Sequence 48, Appl
43	16	26.7	55	10	US-09-977-406A-49	Sequence 49, Appl
44	16	26.7	56	10	US-09-977-406A-50	Sequence 50, Appl
45	16	26.7	57	10	US-09-977-406A-51	Sequence 51, Appl

ALIGNMENTS

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RESULT 1
US-09-977-406A-92
; Sequence 92, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from PCX145 sequence (polypeptide analog)
US-09-977-406A-92

Query Match      100.0%; Score 60; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-59;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 EMQTDNCETCTCYETEMQTDNCETCTCYETEMQTDNCETCTCYET 60

RESULT 2
US-09-977-406A-91
; Sequence 91, Application US/09977406A

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Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 91
LENGTH: 45
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-91

Query Match 75.0%; Score 45; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.9e-43;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEMQDNCETCTCYETEMQDNCETCTCYET 45
DB 1 EMQDNCETCTCYETEMQDNCETCTCYETEMQDNCETCTCYET 45

RESULT 3
US-09-977-406A-90
Sequence 90, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 90
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from PCK3145 sequence (polypeptide analog)
US-09-977-406A-90

Query Match 50.0%; Score 30; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-26;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETEMQDNCETCTCYET 30
DB 1 EMQDNCETCTCYETEMQDNCETCTCYET 30

RESULT 4
US-09-977-406A-10
Sequence 10, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHufSP94 sequence (polypeptide analog)
US-09-977-406A-10

Query Match 26.7%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 5
US-09-977-406A-11
Sequence 11, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHufSP94 sequence (polypeptide analog)
US-09-977-406A-11

Query Match 26.7%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
DB 1 EMQDNCETCTCYETE 16

RESULT 6
US-09-977-406A-12
Sequence 12, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12

LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406a-12

Query Match 26.7%; Score 16; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETE 16
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Db 1 EMQDNCETCTCYETE 16

RESULT 7
US-09-977-406a-13
Sequence 13, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406a-13

Query Match 26.7%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 EMQDNCETCTCYETE 16

RESULT 8
US-09-977-406a-14
Sequence 14, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406a-14

Query Match 26.7%; Score 16; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 1 EMQDNCETCTCYETE 16

RESULT 9
US-09-977-406a-15
Sequence 15, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406a-15

Query Match 26.7%; Score 16; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMQDNCETCTCYETE 16
|||||
Db 1 EMQDNCETCTCYETE 16

RESULT 10
US-09-977-406a-16
Sequence 16, Application US/09977406A
Publication No. US20030170220A1
GENERAL INFORMATION:
APPLICANT: PROCYON BIOPHARMA INC.
TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITTING TUMORS
FILE REFERENCE: 06508-030-US-03
CURRENT APPLICATION NUMBER: US/09/977,406A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: CA 2,321,256
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: CA 2,355,334
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polypeptide derived from rHUSP94 sequence (polypeptide analog)
US-09-977-406a-16

Query Match 26.7%; Score 16; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EMQDNCETCTCYETE 16

RESULT 11
US-09-977-406A-17
; Sequence 17, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-17

Query Match 26.7%; Score 16; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
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DB 1 EMQDNCETCTCYETE 16

RESULT 12
US-09-977-406A-18
; Sequence 18, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-18

Query Match 26.7%; Score 16; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.1e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
DB 1 EMQDNCETCTCYETE 16

RESULT 13
US-09-977-406A-19
; Sequence 19, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:

; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-19

Query Match 26.7%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.2e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
DB 1 EMQDNCETCTCYETE 16

RESULT 14
US-09-977-406A-20
; Sequence 20, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-20

Query Match 26.7%; Score 16; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.4e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
|||
DB 1 EMQDNCETCTCYETE 16

RESULT 15
US-09-977-406A-21
; Sequence 21, Application US/09977406A
; Publication No. US20030170220A1
; GENERAL INFORMATION:
; APPLICANT: PROCYON BIOPHARMA INC.
; TITLE OF INVENTION: PHARMACEUTICAL PREPARATIONS AND METHODS FOR INHIBITING TUMORS
; FILE REFERENCE: 06508-030-US-03
; CURRENT APPLICATION NUMBER: US/09/977,406A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: CA 2,321,256
; PRIOR FILING DATE: 2000-10-16

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; PRIOR APPLICATION NUMBER: CA 2,355,334
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide derived from rHuSP94 sequence (polypeptide analog)
US-09-977-406A-21

```

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Query Match          26.7%; Score 16; DB 10; Length 27;
Best Local Similarity 100.0%; Pred.No. 4.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EMQTDNCETCTCYETE 16
    |||||
Db 1 EMQTDNCETCTCYETE 16

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Search completed: May 4, 2005, 15:24:09
 Job time : 66.9818 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 14:12:38 ; Search time 21.6 Seconds
(without alignments)
267.269 Million cell updates/sec

Title: US-09-977-406A-92

Perfect score: 60

Sequence: 1 EMQTDNCETCTCYETEMQTD.....TCYETEMQTDNCETCTCYET 60

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	26.7	114	2 A34567	beta-microseminopr
2	6	10.0	326	2 UC7094	nine-heme cytochr
3	6	10.0	601	2 B96744	unknown protein [i
4	6	10.0	895	2 T32374	hypothetical prote
5	6	10.0	1045	2 A29840	serine proteinase
6	5	8.3	38	2 JN0613	defensin 4K - scor
7	5	8.3	38	2 S27242	defensin - blue da
8	5	8.3	83	2 S51116	methionine adenosy
9	5	8.3	91	2 S52089	transcription fact
10	5	8.3	114	2 A54663	seminal plasma pro
11	5	8.3	119	1 S73864	hypothetical prote
12	5	8.3	127	2 B69429	conserved hypotet
13	5	8.3	130	2 G65019	hypothetical prote
14	5	8.3	135	2 F81108	toxin-activating p
15	5	8.3	167	2 C86241	protein t16B5.9 [i
16	5	8.3	210	2 AC2316	transposase alr408
17	5	8.3	226	2 C70962	hypothetical prote
18	5	8.3	246	2 A81679	conserved hypotet
19	5	8.3	256	2 T05554	hypothetical prote
20	5	8.3	281	2 A11064	probable outer mem
21	5	8.3	287	2 S76738	hypothetical prote
22	5	8.3	295	2 S76790	hypothetical prote
23	5	8.3	301	2 T26546	hypothetical prote
24	5	8.3	315	2 S66038	vac protein - Bac
25	5	8.3	317	2 C93452	hypothetical prote
26	5	8.3	319	1 T50370	transcription fact
27	5	8.3	322	2 C70905	hypothetical prote
28	5	8.3	334	2 D82803	glyceroldehyde-3-P
29	5	8.3	339	2 T16273	hypothetical prote

30	5	8.3	340	1 B55973	transcription fact
31	5	8.3	347	2 AC0825	anaerobic sulfite
32	5	8.3	347	2 A38453	anaerobic sulfite
33	5	8.3	349	1 T50359	transcription fact
34	5	8.3	358	1 A55973	transcription fact
35	5	8.3	358	1 A51735	transcription fact
36	5	8.3	359	1 T51734	transcription fact
37	5	8.3	360	1 A55198	transcription fact
38	5	8.3	360	2 T06592	methionine adenosy
39	5	8.3	361	2 T50505	gene wnt8 protein
40	5	8.3	363	1 C55973	transcription fact
41	5	8.3	366	2 S66351	methionine adenosy
42	5	8.3	374	2 S41758	heat shock protein
43	5	8.3	374	2 C97058	molecular chaperon
44	5	8.3	385	2 C93817	coproporphyrinogen
45	5	8.3	390	2 S46540	methionine adenosy

ALIGNMENTS

RESULT 1
A34567
beta-microseminoprotein precursor - human
N:Alternate names: beta-inhibin; prostatic secretory protein; PSP-94; seminal plasma pro
C:Species: Homo sapiens (man)
C>Date: 13-Jul-1990 #sequence revision 13-Jul-1990 #text change 09-Jul-2004
C:Accession: A34567; A26451; A29777; A30984; A60673; S16238; I52682
R:Green, C.B.; Liu, W.Y.; Kwok, S.C.M.
Biochem. Biophys. Res. Commun. 167, 1184-1190, 1990
A>Title: Cloning and nucleotide sequence analysis of the human beta-microseminoprotein g
A:Reference number: A34567; MUID:90211299; PMID:2322265
A:Accession: A34567
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-114 <GRE>
A:Cross-references: UNIPROT:P06118; GB:M34376; NID:G514370; PID:AA59871.1; PID:G514372
R:Mokay, M.; Nolte, S.; Fournier, S.; Benjannet, S.; Chadelaine, P.; Paradis, G.; Dube
DNA 6, 23-29, 1987
A>Title: Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma p
A:Reference number: A26451; MUID:87161231; PMID:3829888
A:Accession: A26451
A:Molecule type: mRNA
A:Residues: 1-114 <MBI>
A:Cross-references: GB:M15865; NID:G338414; PID:AAA36635.1; PID:G338415
R:Akiyama, K.; Yoshioke, Y.; Schmid, K.; Offner, G.D.; Troxler, R.F.; Tuda, R.; Hara, M
Biochim. Biophys. Acta 829, 288-294, 1985
A>Title: The amino acid sequence of human beta-microseminoprotein.
A:Reference number: A29777; MUID:85199974; PMID:3995056
A:Accession: A29777
A:Molecule type: Protein
A:Residues: 21-58; 'PT', 61-113 <AKI>
R:Seidah, N.G.; Arabaci, N.J.; Rochement, J.; Sheth, A.R.; Chretien, M.
FEBS Lett. 175, 349-355, 1984
A>Title: Complete amino acid sequence of human seminal plasma beta-inhibin. Prediction o
A:Reference number: A30984; MUID:85004133; PMID:6434350
A:Accession: A30984
A:Molecule type: Protein
A:Residues: 21-112; 'G', 114 <SEI>
R:Weiber, H.; Andersson, C.; Murne, A.; Rannevik, G.; Lindstroem, C.; Lilja, H.; Fernlund
Am. J. Pathol. 137, 593-604, 1990
A>Title: Beta microseminoprotein is not a prostate-specific protein.
A:Reference number: A60673; MUID:90379237; PMID:2205099
A:Accession: A60673
A:Molecule type: protein
A:Residues: 21; 'X', 23-34 <WEI>
R:Nolte, S.; Mikiy, M.; Chretien, M.
Biochim. Biophys. Acta 1089, 247-249, 1991
A>Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in
A:Reference number: S16237; MUID:91274357; PMID:2054385
A:Accession: S16238
A:Molecule type: DNA

A/Residues: 1-114 <NOT>
 A/Cross-references: EMBL:X57928; NID:935760; PIDN:CAA1002.1; PID:9825707
 A/Note: the authors translated the codon ACT for residue 54 as TTP
 R/Liu, A.Y.; Brader, R.C.; Vessella, R.L.
 Cancer Lett. 74, 91-99, 1993
 A/Title: Decreased expression of prostatic secretory protein PSP94 in prostate cancer.
 A/Reference number: 152682; MUID:94115955; PMID:7506990
 A/Accession: 152682
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-114 <RES>
 A/Cross-references: GB:567815; NID:9460568; PIDN:AA29732.1; PID:9460569
 C/Comment: This protein is a component of seminal plasma as well as secretory fluids from
 A/Gene: GDB:MSMB
 A/Cross-references: GDB:128042; OMIM:157145
 A/Map position: 10q11.2-10q11.2
 A/Intons: 1/3; 37/1; 72/2
 C/Superfamily: seminal plasma protein
 C/Keywords: semen
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-114/Product: seminal plasma protein #status experimental <MAT>

Query Match 26.7%; Score 6; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMQDNCETCTCYETE 16
 DB 51 EMQDNCETCTCYETE 66

RESULT 2
 JC7094
 nine-heme cytochrome c - Desulfovibrio desulfuricans
 C/Species: Desulfovibrio desulfuricans
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: JC7094
 R/Saraiya, L.M.; da Costa, P.N.; Legall, J.
 Biochem. Biophys. Res. Commun. 262, 629-634, 1999
 A/Title: Sequencing the gene encoding desulfovibrio desulfuricans ATCC 27774 nine-heme c
 A/Reference number: JC7094; MUID:99400433; PMID:10473375
 A/Accession type: DNA
 A/Molecule type: DNA
 A/Residues: 1-326 <SAR>
 A/Cross-references: UNIPROT:Q9RNB6; GB:AF186393; NID:95924394; PIDN:AA256586.1; PID:9592
 A/Experimental source: ATCC 27774
 C/Genetics:
 A/Gene: 9HCC
 C/Keywords: electron transfer; heme; heme binding

Query Match 10.0%; Score 6; DB 2; Length 326;
 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DNCETC 10
 DB 75 DNCETC 80

RESULT 3
 B96744
 unknown protein [imported] - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C/Accession: B96744
 R/Theologis, A.; Becker, J.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hitzar, L.
 Nature 408, 816-820, 2000
 A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luroe, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.M.
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A/Reference number: A86141; MUID:21016719; PMID:11130712
 A/Accession: B96744

A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-601 <STO>
 A/Cross-references: UNIPROT:Q9C7H2; GB:AE005173; NID:911054407; PIDN:AA27794.1; GSPDB:GP
 C/Genetics:
 A/Gene: P28P5.4
 A/Map position: 1

Query Match 10.0%; Score 6; DB 2; Length 601;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CECTTC 12
 DB 514 CECTTC 519

RESULT 4
 T32374
 hypothetical protein K10F12.3 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2000
 C/Accession: T32374
 R/Wohlmann, P.; Beck, C.
 submitted to the EMBL Data Library, September 1997
 A/Description: The sequence of C. elegans cosmid K10F12.
 A/Reference number: Z21157
 A/Accession: T32374
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-895 <WOH>
 A/Cross-references: EMBL:AF025462; PIDN:AA271005.1; GSPDB:GN00021; CESP:K10F12.3
 A/Experimental source: strain Bristol N2; clone K10F12
 C/Genetics:
 A/Gene: CESP:K10F12.3
 A/Map position: 3
 A/Intons: 46/1; 96/1; 124/3; 165/1; 223/3; 282/3; 340/3; 381/1; 485/3; 516/2; 549/1; 624
 C/Superfamily: yeast 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; 1-phospho
 sphodiesterase domain y homology
 F:338-487/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom

Query Match 10.0%; Score 6; DB 2; Length 895;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCET 9
 DB 288 TDNCET 293

RESULT 5
 A29840
 serine proteinase (EC 3.4.21.-) precursor - Serratia marcescens (strain IFO-3046)
 C/Species: Serratia marcescens
 C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
 C/Accession: A29840
 R/Yanagida, N.; Uozumi, T.; Beppu, T.
 J. Bacteriol. 166, 937-944, 1986
 A/Title: Specific excretion of Serratia marcescens protease through the outer membrane of
 A/Reference number: A29840; MUID:86223815; PMID:3011754
 A/Accession: A29840
 A/Molecule type: DNA
 A/Residues: 1-1045 <YAN>
 A/Cross-references: UNIPROT:P09489; GB:M13469; NID:9152857; PIDN:AA26572.1; PID:9152858
 C/Superfamily: autotransporter subtilisin-like protease precursor; subtilisin homology
 C/Keywords: hydrolase; serine proteinase
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-408/Product: serine proteinase #status predicted <MAT>

F:67-355/Domain: subtilisin homology <SBT>
F:409-1045/Domain: carboxyl-terminal propeptide #status predicted <Pro>
F:76,112,341/Active site: Asp, His, Ser #status predicted

Query Match 10.0%; Score 6; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TEMOTD 20
Db 953 TEMOTD 958

RESULT 6
JN0613
defensin 4K - scorpion (leirus quinquestriatus)

N/Alternate names: antibacterial 4K peptide
C/Species: Leirus quinquestriatus hebraeus
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: JN0613

R/Coclanich, S.; Goyffon, M.; Bontems, F.; Bulet, P.; Bouet, F.; Menez, A.; Hoffmann, J.
Biochem. Biophys. Res. Commun. 194, 17-22, 1993
A/Title: Purification and characterization of a scorpion defensin, a 4kDa antibacterial
A/Reference number: JN0613; MUID:93326112; PMID:8333834
A/Accession: JN0613

A/Molecule type: protein

A/Residues: 1-38 <COC>

A/Cross-references: UNIPROT:P41965

A/Note: this protein is similar to scorpion toxins and insect defensins

Query Match 8.3%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TCTCY 13
Db 32 TCTCY 36

RESULT 7

S27242
defensin - blue darter

C/Species: Aeschna cyanea (blue darter)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S27242

R/Bulet, P.; Coclanich, S.; Reuland, M.; Sauber, F.; Bischoff, R.; Hegy, G.; van Dorssse
Eur. J. Biochem. 209, 977-984, 1992

A/Title: A novel insect defensin mediates the inducible antibacterial activity in larvae
A/Reference number: S27242; MUID:93049356; PMID:1425705

A/Accession: S27242

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-38 <BUL>

A/Cross-references: UNIPROT:P80154

Query Match 8.3%; Score 5; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 TCTCY 13
Db 33 TCTCY 37

RESULT 8

S53116
methionine adenosyltransferase (BC 2.5.1.6) - chickpea (fragment)

N/Alternate names: S-adenosylmethionine synthetase

C/Species: Cicer arietinum (chickpea, garbanzo)

C/Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: S53116

R/Cervantes, E.
submitted to the EMBL Data Library, March 1995

A/Reference number: S53116

A/Accession: S53116

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-83 <CER>

A/Cross-references: UNIPROT:Q39465; EMBL:X85252; NID:g1808591; PIDN:CAA59508.1; PID:g732

C/Superfamily: methionine adenosyltransferase

C/Keywords: S-adenosylmethionine; transferase

Query Match 8.3%; Score 5; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CETCT 11
Db 43 CETCT 47

RESULT 9
S52089

transcription factor isl-2a (clone S3) - chinook salmon

N/Alternate names: insulin enhancer-binding protein isl-2a; islct-2a protein

C/Species: Oncorhynchus tshawytscha (chinook salmon)

C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 15-Oct-1999
C/Accession: S52089

R/Gong, Z.; Hew, C.L.

Biochim. Biophys. Acta 1260, 349-354, 1995

A/Title: Several splicing variants of isl-1 like genes in the chinook salmon (Oncorhynch

A/Reference number: S52089; MUID:95178560; PMID:7873614

A/Accession: S52089

A/Molecule type: mRNA

A/Residues: 1-91 <GON>

A/Cross-references: EMBL:X64882

A/Experimental source: clone S3

C/Genetics:

A/Gene: isl-2a

C/Superfamily: transcription factor isl-1; homeobox homology; LIM metal-binding repeat h

C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati

F:3-56/Domain: LIM metal-binding repeat homology <LIM>

Query Match 8.3%; Score 5; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 ETCCT 12
Db 40 ETCCT 44

RESULT 10

A54663
seminal plasma protein PSP-94 precursor - rhesus macaque

N/Alternate names: prostatic secretory protein PSP94

C/Species: Macaca mulatta (rhesus macaque)

C/Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C/Accession: S16237; A54663

R/Notet, S.; Mdkay, M.; Chretien, M.

Biochim. Biophys. Acta 1089, 247-249, 1991

A/Title: Prostatic secretory protein PSP(94): gene organization and promoter sequence in

A/Reference number: S16237; MUID:91274357; PMID:2054385

A/Accession: S16237

A/Molecule type: DNA

A/Residues: 1-114 <NO2>

A/Cross-references: UNIPROT:P25142; EMBL:X57932; NID:g38094; PIDN:CAA41003.1; PID:g82915;

A/Note: the authors translated the codon ACT for residue 54 as Trp

R/Notet, S.; St-Louis, D.; Mdkay, M.; Chretien, M.

Genomics 9, 775-777, 1991

A/Title: Rapid evolution of prostatic protein PSP-94 suggested by sequence divergence bet

A/Reference number: A54663; MUID:91244325; PMID:2037304

A/Accession: A54663

A/Molecule type: mRNA

A/Residues: 1-114 <NOL>

A/Cross-references: GB:M92161; NID:g342280; PIDN:AAA36903.1; PID:g342281

C:Genetics:

A:Introns: 1/3; 37/1: 72/2
C:Superfamily: seminal plasma protein
F:1-20/Domain: signal sequence #status predicted <SIG>

Query Match

Best Local Similarity 8.3%; Score 5; DB 2; Length 114;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8
DB 54 TDNCE 58

RESULT 11

S73864
hypothetical protein H10.orf119 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S73864

R:Himmelreich, R.; Hilbert, H.; Piagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996

A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73864

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-119 <HTM>

A:Cross-references: UNIPROT:P75480; EMBL:AE000052; GB:U00089; NID:91674223; PIDN:AMB9618
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C:Genetics:

A:Genetic code: SGCG

C:Superfamily: holo-ACP synthase

Query Match

Best Local Similarity 8.3%; Score 5; DB 1; Length 119;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QTDNC 7
DB 21 QTDNC 25

RESULT 12

B69429
conserved hypothetical protein AF1438 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: B69429

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69429

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-127 <KLE>

A:Cross-references: UNIPROT:Q28834; GB:AE001004; GB:AE000782; NID:92689327; PIDN:AMB981

Query Match 8.3%; Score 5; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 50;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CYETE 16
DB 16 CYETE 20

RESULT 13

G65019
hypothetical protein b2448 - Escherichia coli (strain K-12)
C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: G65019

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G65019

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-130 <BLAT>

A:Cross-references: UNIPROT:P76548; GB:AE000332; GB:U00096; NID:91788789; PIDN:AACT5501.
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli hypothetical protein b2448

Query Match

Best Local Similarity 8.3%; Score 5; DB 2; Length 130;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCE 8
DB 43 TDNCE 47

RESULT 14

F81108
toxin-activating protein, probable NMB1210 [imported] - Neisseria meningitidis (strain MC
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C/Accession: F81108
R:Teitelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000

A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81108

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <TEM>

A:Cross-references: UNIPROT:Q9JZB0; GB:AE002469; GB:AE002098; NID:97226446; PIDN:AAFA159;
A:Experimental source: serogroup B, strain MC58
C:Genetics:

A:Gene: NMB1210

C:Superfamily: hemolysin C

Query Match 8.3%; Score 5; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 59;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ETENQ 18
DB 80 ETENQ 84

RESULT 15

C86241
protein T16B5.9 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: C86241

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A6141; MUID:21016719; PMID:11130712
A/Accession: C96241
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-167 <STO>
A/Cross-references: UNIPROT:Q9SAC5; GB:AE005172; NID:g4874271; PIDN:AAD31336.1; GSPDB:GN
C:Genetics:
A/Gene: T16B5.9
A/Map position: 1

Query Match 8.3%; Score 5; DB 2; Length 167;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TCYET 15
|||
Db 91 TCYET 95

Search completed: May 4, 2005, 14:34:58
Job time : 22.6 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 4, 2005, 14:04:27 ; Search time 102.982 Seconds
(without alignments)
298.351 Million cell updates/sec

Title: US-09-977-406a-92
Perfect score: 60
Sequence: 1 EWQTDNCETCTCYETEMQTD.....TCYETEMQTDNCETCTCYET 60

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	26.7	114	1 MSMB_HUMAN	P08118 homo sapien
2	7	11.7	114	1 MSMB_PAPAN	Q28767 papio anubi
3	6	10.0	196	2 Q9D8T1	Q948Y1 mus musculu
4	6	10.0	215	2 Q7V5F4	Q7V5F4 prochloroco
5	6	10.0	326	1 CYC9_DESDE	Q9Yn68 desulfovibr
6	6	10.0	459	1 MURD_LACPL	Q86V80 lactobacill
7	6	10.0	601	2 Q9C7H2	Q9C7H2 arabidopsis
8	6	10.0	1045	1 PRTS_SERMA	P09489 serraria ma
9	6	10.0	1068	2 Q81A76	Q81A76 caenorhabdi
10	6	10.0	1075	2 Q81A75	Q81A75 caenorhabdi
11	6	10.0	1615	2 Q7QZU9	Q7QZU9 giardia lam
12	6	10.0	1870	2 Q7OH34	Q7OH34 fowlpox vir
13	6	10.0	1870	2 Q9J5A0	Q9J5A0 fowlpox vir
14	6	10.0	3110	1 LMA2_HUMAN	P24043 homo sapien
15	5	8.3	37	1 DEF4_ANDAV	P56686 androctonus
16	5	8.3	38	1 DEF4_LEIGH	P41965 leiturus qui
17	5	8.3	38	1 DEF1_AESCY	P80154 aescyna cya
18	5	8.3	51	2 Q7V3N1	Q7V3N1 enterobacte
19	5	8.3	54	2 Q24985	Q24985 giardia lam
20	5	8.3	58	2 Q8RXC2	Q8RXC2 escherichia
21	5	8.3	70	2 Q8R5C3	Q8R5C3 mus musculu
22	5	8.3	74	1 DEF1_DERVA	Q86q15 dermatocor
23	5	8.3	74	2 Q86LE4	Q86LE4 boophilus m
24	5	8.3	75	2 Q8JX66	Q8JX66 sen virus.
25	5	8.3	75	2 Q8JX67	Q8JX67 sen virus.
26	5	8.3	77	2 Q8C1L6	Q8C1L6 mus musculu
27	5	8.3	81	2 Q6Y776	Q6Y776 bacterioph
28	5	8.3	83	2 Q39465	Q39465 cicer arlet
29	5	8.3	105	2 Q8BU77	Q8BU77 mus musculu
30	5	8.3	110	2 Q42169	Q42169 arabidopsis
31	5	8.3	111	2 Q9JH97	Q9JH97 unclassified

32	5	8.3	112	2 Q854B7	Q854B7 mycobacteri
33	5	8.3	113	2 Q22079	Q22079 nicotiana t
34	5	8.3	114	1 MSMB_MACMU	P25142 macaca mla
35	5	8.3	114	2 Q8L2K3	Q8L2K3 helicobacte
36	5	8.3	115	2 Q7KTX0	Q7KTX0 dirosophila
37	5	8.3	117	2 Q8A7Y2	Q8A7Y2 bacteroides
38	5	8.3	119	1 ACPS_MYCPN	P75480 mycoplasma
39	5	8.3	121	2 Q7ZGB3	Q7ZGB3 human immun
40	5	8.3	127	2 Q28834	Q28834 archaeoglob
41	5	8.3	127	2 Q6IKD4	Q6IKD4 dirosophila
42	5	8.3	130	1 YFQO_ECOLI	P76548 escherichia
43	5	8.3	131	2 Q8CFP4	Q8CFP4 mus musculu
44	5	8.3	132	2 Q97442	Q97442 giardia lam
45	5	8.3	133	2 Q6PRE3	Q6PRE3 helicobacte

ALIGNMENTS

RESULT 1	MSMB_HUMAN	STANDARD	PRT	114 AA.
AC	P08118; P11999; Q13125; Q9UC59;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Beta-microseminoprotein precursor (Prostate secreted seminal plasma protein) (Prostate secretory protein PSP94) (PSP-94) (Seminal plasma beta-inhibin) (Immunoglobulin binding factor) (IGBF) (PN44).			
GN	Name=MSMB; Synonyms=PRSP;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87161231; PubMed=3829888;			
RA	Molloy M., Nolet S., Fournier S., Benjannet S., Chapdelaine P., Paradis G., Dube J.Y., Tremblay R., Lazure C., Seidah N.G., Chretien M.;			
RT	"Molecular cloning and sequence of the cDNA for a 94-amino-acid seminal plasma protein secreted by the human prostate.";			
RL	DNA 6:23-29(1987).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91274357; PubMed=2054385; DOI=10.1016/0167-4781(91)90016-F;			
RA	Nolet S., Molloy M., Chretien M.;			
RT	"Prostatic secretory protein PSP94: gene organization and promoter sequence in rhesus monkey and human.";			
RL	Biochim. Biophys. Acta 1089:247-249(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90211299; PubMed=2322265;			
RA	Green C.B., Liu W.Y., Kwok S.C.M.;			
RT	"Cloning and nucleotide sequence analysis of the human beta-microseminoprotein gene.";			
RL	Biochem. Biophys. Res. Commun. 167:1184-1190(1990).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90073664; PubMed=2590204;			
RA	Uvshack M., Lindstrom C., Weiber H., Abrahamson P.-A., Lilja H., Lundwall A.;			
RT	"Molecular cloning of a small prostate protein, known as beta-microseminoprotein, PSP94 or beta-inhibin, and demonstration of transcripts in non-genital tissues.";			
RL	Biochem. Biophys. Res. Commun. 164:1310-1315(1989).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=94115955; PubMed=7506990; DOI=10.1016/0304-3835(93)90049-F;			
RA	Liu A.Y., Bradner R.C., Vessella R.L.;			
RT	"Decreased expression of prostatic secretory protein PSP94 in prostate cancer.";			

RL Cancer Lett. 74:91-99(1993).
 RP [6]
 RA SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
 RC TISSUE=Prostate; PubMed=7566962;
 RX MEDLINE=9603256;
 RA Xuan J.W., Chin J.D., Guo Y., Chambers A.F., Finkelstein M.A.,
 RA Clarke M.W.;
 RT "Alternative splicing of PSP94 (prostatic secretory protein of 94
 RT amino acids) mRNA in prostate tissue.";
 RL Oncogene 11:1041-1047(1995).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Balaji-Gupta M., Clarke M.W.;
 RT "Prostate specific protein (PSP94) expression in a human endometrial
 RT cell line (KLE)." ;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rosa S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bese S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.U., Huix S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hulton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Klein J.E., Jones S.J.M., Skalska U., Smilins D.E.,
 RA Schnerch A., Schen J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 2-72 FROM N.A.
 RX MEDLINE=99421644; PubMed=10491085;
 RA Maekinen M., Valtanen-Andre C., Lundwall A.;
 RT "New world, but not old world, monkeys carry several genes encoding
 RT beta-microseminoprotein.";
 RL Eur. J. Biochem. 264:407-414(1999).
 RN [10]
 RP SEQUENCE OF 21-113
 RX MEDLINE=8519974; PubMed=3995056; DOI=10.1016/0167-4838(85)90200-6;
 RA Akiyama K., Yoshiooka Y., Schmidt K., Offner G.D., Troxler R.F.,
 RA Tada R., Hara M.;
 RT "The amino acid sequence of human beta-microseminoprotein.";
 RL Biochim. Biophys. Acta 829:288-294(1985).
 RN [11]
 RP SEQUENCE OF 21-114
 RX MEDLINE=85004133; PubMed=6433350; DOI=10.1016/0014-5793(84)80766-8;
 RA Seidh N.G., Arbatli N.J., Rochement J., Sheh A.R., Chretien M.;
 RT "Complete amino acid sequence of human seminal plasma beta-inhibin.
 RT Prediction of post Glu-Arg cleavage as a maturation site.";
 RL FEBS Lett. 175:349-355(1984).
 RN [12]
 RP SEQUENCE OF 21-50 AND 113-114.
 RX MEDLINE=92028964; PubMed=1930232;
 RA Liang Z.G., Kamada M., Koide S.S.;
 RT "Structural identity of immunoglobulin binding factor and prostatic
 RT secretory protein of human seminal plasma.";
 RL Biochem. Biophys. Res. Commun. 180:356-359(1991).
 RN [13]
 RP SEQUENCE OF 21-41, AND TISSUE SPECIFICITY.
 RC TISSUE=Semen;
 RX MEDLINE=95401076; PubMed=7671139; DOI=10.1016/1357-2725(95)00021-G;
 RA Ohkubo I., Tada T., Ochiai Y., Ueyama H.,imoto T., Sasaki M.;

RT "Human seminal plasma beta-microseminoprotein: its purification,
 RT characterization, and immunohistochemical localization.";
 RL Int. J. Biochem. Cell Biol. 27:603-611(1995).
 RN [14]
 RP SEQUENCE OF 21-32.
 RX MEDLINE=21648993; PubMed=11788998;
 RA DOI=10.1002/1615-9861(200201)21:1<112::AID-PROT112>3.3.CO;2-E;
 RA Ghafouri B., Stabhorn B., Tegesson C., Lindahl M.;
 RT "Newly identified proteins in human nasal lavage fluid from non-
 RT smokers and smokers using two-dimensional gel electrophoresis and
 RT peptide mass fingerprinting.";
 RL Proteomics 2:112-120(2002).
 CC -1- SUPPLEMENTAL LOCATIONS: Secreted. Sperm surface.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=PSP94;
 CC IsoId=P08118-1; Sequence=Displayed;
 CC Name=PSP57;
 CC IsoId=P08118-2; Sequence=VSP 003275, VSP 003276;
 CC -1- TISSUE SPECIFICITY: Strongly expressed in prostate, liver, kidney,
 CC breast and penis. Also expressed in pancreas, esophagus, stomach,
 CC duodenum, colon, trachea, lung, salivary glands and fallopian
 CC tube. PSP94 is expressed in lung and breast, whereas PSP57 is
 CC found in kidney and bladder.
 CC -1- MISCELLANEOUS: Specific receptors for this protein are found on
 CC spermatozoa and in the prostate.
 CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
 CC -1- CAUTION: Was originally thought to inhibit the secretion of FSH by
 CC pituitary cells.
 CC -----
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 DR EMBL: M34376; AAA59871.1; -
 DR EMBL: M34373; AAA59871.1; JOINED.
 DR EMBL: M34374; AAA59871.1; JOINED.
 DR EMBL: M34375; AAA59871.1; JOINED.
 DR EMBL: M15885; AAA66355.1; -
 DR EMBL: X57928; CAA41002.1; -
 DR EMBL: X57929; CAA41002.1; JOINED.
 DR EMBL: X57930; CAA41002.1; JOINED.
 DR EMBL: X57931; CAA41002.1; JOINED.
 DR EMBL: S67815; AAB29732.1; -
 DR EMBL: U22178; AAA83556.1; -
 DR EMBL: U78976; AAB37355.1; -
 DR EMBL: BC005257; AAH05257.1; -
 DR EMBL: AJ13356; CAB39325.1; -
 DR PIR: A34567; A34567.
 DR PIR: G01730; G01730.
 DR GeneW: HGNC:7372; MSMB.
 DR H-InvDB: HIX0008822; -
 DR GIM: 157145; -
 DR GO: GO:0005615; Cextracellular space; TAS.
 DR GO: GO:0005634; Cnucleus; TAS.
 DR InterPro: IPR008735; PSP94.
 DR Pfam: PF05825; PSP94; 1.
 DR Alternative splicing; Direct protein sequencing; Polymorphism; Signal.
 KW SIGNAL
 FT CHAIN 1 20
 FT DISULFID 21 114
 FT DISULFID 22 38
 FT DISULFID 57 93
 FT DISULFID 60 69
 FT DISULFID 62 70
 FT DISULFID 70 70
 FT DISULFID 84 107
 FT VARSPLIC 37 77
 FT
 FT -> MFHLMWTKTKAKSSRRRISISMRRRROKRPVLS
 FT VNG (in isoform PSP57).
 FT /FTid=VSP_003275.

Thu May 5 15:11:17 2005

```

FT VASBPIC 78 114 Missing (in isoform PSP57).
FT /FTID=VSP_003276.
Query March 26.7% Score 16; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EMOTDNCETCTCYETE 16
| | | | | | | | | | | | | | | |
Db 51 EMOTDNCETCTCYETE 66

RESULT 2
MSMB_PAPAN STANDARD; PRT; 114 AA.
AC 028757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-microseminoprotein precursor (Prostate secreted seminal plasma
DE protein) (Prostate secretory protein PSP94) (PSP-94).
GN Name=MSMB; Synonyms=PSP94;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OC NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=97316893; PubMed=9174167;
RA Xuan J.W., Wu D., Guo Y., Garde S., Shum D.T., Molkay M., Zhong R.,
RA Chin J.L.;
RT "Molecular cloning and gene expression analysis of PSP94 (prostate
RT secretory protein of 94 amino acids) in primates.";
RL DNA Cell Biol. 16:627-638(1997).
CC -1- SUBCELLULAR LOCATION: Secreted. Sperm surface (By similarity).
CC -1- SIMILARITY: Belongs to the beta-microseminoprotein family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; U49786; AAB62726.1; -.
DR InterPro; IPR008735; PSP94.
DR Pfam; PF05825; PSP94; 1.
KW SIGNAL.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 114 Beta-microseminoprotein.
FT DISULFID 22 38 By similarity.
FT DISULFID 57 93 By similarity.
FT DISULFID 60 69 Or C-60 with C-70 (By similarity).
FT DISULFID 62 70 Or C-62 with C-69 (By similarity).
FT DISULFID 84 107 By similarity.
SQ SEQUENCE 114 AA; 13013 MW; A08C837ED81F98BD CRC64;

Query March 11.7% Score 7; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 WQDNCNE 8
| | | | | | | |
Db 52 WQDNCNE 58

RESULT 3
Q9DBY1 PRELIMINARY; PRT; 196 AA.
AC Q9DBY1;

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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 29, Last annotation update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:1810020E01 product: hypothetical protein, full insert
DE sequence (Riken cDNA 1810020E01).
DE Name=1810020E01Rik;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium;
RT "The FANTOM Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Komori H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanaki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komori H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki C., Sakai K.,
RA Matsuyama T., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A.

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RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien P.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK007559; BAB5107.1; -
 DR EMBL; BC023171; AAH23171.1; -
 DR MGI; MGI:1913521; 1810020501Rik.
 DR GO; GO:0016021; C:integral to membrane; TMS.
 DR InterPro; IPR009801; DUF1370.
 DR Pfam; PF07114; DUF1370; 1.
 DR Hypothetical protein.
 KM SEQUENCE 196 AA; 21539 MM; 994D5E2251C5FB CRC64;
 SQ
 Query Match 10.0%; Score 6; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 NCERTCT 11
 DB 98 NCERTCT 103
 RESULT 4
 07V5F4 PRELIMINARY; PRT; 215 AA.
 AC 07V5F4;
 DT 01-OCT-2003 (TEMBLrel. 25, Created)
 DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Bacterial regulatory proteins, Asnc family.
 GN OrderedLocustNames=PM1607;
 OS Prochlorococcus marinus (Strain MIT 9313).
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcales;
 OC Prochlorococcus.
 OC NCBI_TaxID=74547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22855693; PubMed=12917642; DOI=10.1038/nature01947;
 RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
 RA Aillegren N.A., Arriaga A., Coleman A., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinner E.R., Chisholm S.W.;
 RT "Genomic divergence in two Prochlorococcus ecotypes reflects oceanic
 RT niche differentiation.";
 RL Nature 424:1042-1047(2003).
 DR EMBL; BX572099; CAE21782.1;
 DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
 KM Complete proteome.
 SQ SEQUENCE 215 AA; 24165 MM; E663AA68A216D0C5 CRC64;

Query Match 10.0%; Score 6; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 YETEMQ 18
 DB 142 YETEMQ 147
 RESULT 5
 CYC9 DESDE STANDARD; PRT; 326 AA.
 AC 09RN68;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Nine-heme cytochrome C precursor (9Hcc).
 OS Desulfovibrio desulfuricans.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OC NCBI_TaxID=876;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99400423; PubMed=10471375; DOI=10.1006/birc.1999.1238;
 RA Saraiya L.M., da Costa P.N., Legall J.;
 RT "Sequencing the gene encoding Desulfovibrio desulfuricans ATCC 27774
 RT nine-heme cytochrome C.";
 RL Biochem. Biophys. Res. Commun. 262:629-634(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=20022508; PubMed=10555582;
 RA Matias P.M., Saraiya L.M., Soares C.M., Coelho A.V., Legall J.,
 RA Carondo M.A.;
 RT "Nine-haem cytochrome c from Desulfovibrio desulfuricans ATCC 27774:
 RT primary sequence determination, crystallographic refinement at 1.8 Å
 RT and modelling studies of its interaction with the tetrahaem cytochrome
 RT C3.";
 RL J. Biol. Inorg. Chem. 4:478-494(1999).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RC STRAIN=ATCC 27774;
 RX MEDLINE=99148120; PubMed=10368280; DOI=10.1016/S0969-2126(99)80019-7;
 RA Matias P.M., Coelho R., Pereira I.A.C., Coelho A.V., Thompson A.W.,
 RA Steker L., Legall J., Carondo M.A.;
 RT "The primary and three-dimensional structures of a nine-haem
 RT cytochrome c from Desulfovibrio desulfuricans ATCC 27774 reveal a new
 RT member of the Hmc family.";
 RL Structure 7:119-130(1999).
 CC -1- FUNCTION: May form part of a transmembrane redox complex through
 CC which electrons are transferred to the cytoplasm for reduction of
 CC sulfate.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- DOMAIN: Arranged into two tetraheme clusters and the extra heme 4
 CC is located asymmetrically between the two regions.
 CC -1- PTM: Binds 9 heme groups per subunit.
 CC -1- SIMILARITY: Contains 9 cytochrome c domains.
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 CC or send an email to licences@isb-sib.ch).
 CC EMBL; AF186393; AAD56586.1; -
 DR PIR; JC7094; JC7094.
 DR PDB; 19HC; X-ray; A/B=31-322.
 DR PDB; 10FW; X-ray; A/B=31-326.

DR PDB; 1OXY, X-ray, A/B=31-326.
 DR InterPro; IPR000345; CYC_heme_BS.
 DR InterPro; IPR002322; Cyt CIII.
 DR InterPro; IPR011031; Multiheme_cyt.
 DR Pfam; PF02085; Cytochrom_CIII_1.
 DR PRINTS; PRO0609; CYTOCHROME_C3.
 DR PROSITE; PS51008; MULTIHEME_CYTC; 1.
 DR 3D-structure; Electron transport; Heme; Periplasmic; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 1 326
 FT METAL 31 326
 FT METAL 67 67
 FT METAL 70 70
 FT BINDING 77 77
 FT BINDING 80 80
 FT BINDING 81 81
 FT METAL 82 82
 FT METAL 89 89
 FT BINDING 92 92
 FT METAL 93 93
 FT METAL 111 111
 FT BINDING 127 127
 FT BINDING 130 130
 FT METAL 131 131
 FT BINDING 141 141
 FT BINDING 144 144
 FT METAL 145 145
 FT METAL 157 157
 FT BINDING 160 160
 FT METAL 161 161
 FT METAL 227 227
 FT METAL 230 230
 FT METAL 248 248
 FT BINDING 255 255
 FT BINDING 258 258
 FT METAL 259 259
 FT METAL 260 260
 FT BINDING 271 271
 FT BINDING 274 274
 FT METAL 275 275
 FT METAL 294 294
 FT BINDING 297 297
 FT BINDING 300 300
 FT METAL 301 301
 FT BINDING 314 314
 FT BINDING 317 317
 FT METAL 318 318
 FT STRAND 43 46
 FT TURN 55 56
 FT STRAND 63 66
 FT HELIX 67 73
 FT HELIX 77 80
 FT TURN 82 83
 FT HELIX 89 91
 FT TURN 92 92
 FT HELIX 99 101
 FT TURN 102 103
 FT HELIX 106 111
 FT HELIX 127 137
 FT HELIX 139 142
 FT TURN 143 143
 FT HELIX 144 147
 FT HELIX 154 160
 FT STRAND 161 161
 FT TURN 165 166
 FT HELIX 169 177
 FT HELIX 178 178
 FT TURN 182 195
 FT HELIX 204 206
 FT STRAND 211 213
 FT TURN 215 216
 FT STRAND 220 220
 FT STRAND 223 225
 FT HELIX 227 236

FT TURN 237 240
 FT HELIX 242 247
 FT TURN 251 252
 FT HELIX 253 257
 FT TURN 258 258
 FT HELIX 271 274
 FT TURN 281 282
 FT TURN 284 285
 FT HELIX 289 303
 FT TURN 304 305
 FT TURN 311 312
 FT STRAND 320 320
 SQ SEQUENCE 326 AA; 35025 MW; 2ED7025ADDF250E3 CRC64;
 Query Match 10.0%; Score 6; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 DNCETC 10
 Db 75 DNCETC 80
 RESULT 6
 MURD_LACPL STANDARD; PRT; 459 AA.
 AC 088V80;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE UDP-N-acetylmuramoyl-L-alanyl-D-glutamate ligase (BC 6.3.2.9) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase) (D-glutamic acid adding enzyme).
 DE adding enzyme).
 GN Name=murd; OrderedLocNames=lp_2197;
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxId=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCF51;
 RX MEDLINE=22480296; PubMed=1256566; DOI=10.1073/pnas.0337704100;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D., Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M., Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A., Hofter S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B., De Vos W.M., Siezen R.J.;
 RA "Complete genome sequence of Lactobacillus plantarum WCF51.";
 RA Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 RL -1- FUNCTION: Cell wall formation. Catalyzes the addition of glutamate to the nucleotide precursor UDP-N-acetylmuramoyl-L-alanine (UMN) (by similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-L-alanine + glutamate = ADP + phosphate + UDP-N-acetylmuramoyl-L-alanyl-D-glutamate.
 CC -1- PATHWAY: Peptidoglycan biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
 CC -1- SIMILARITY: Belongs to the murCDE family.
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 CC -----
 CC EMBL; AL935258; CAD64544.1; -;
 CC HSSP; P14900; 20AG.
 CC HAMAP; MF_00639; -; 1.
 DR InterPro; IPR004101; Mur_ligase_C.
 DR InterPro; IPR000713; Mur_ligase_N.
 DR InterPro; IPR005762; MurD.

DR Pfam; PF01225; Mur Ligase; 1.
 DR Pfam; PF02875; Mur Ligase C; 1.
 KM ATP-binding; Cell Division; Cell wall; Complete proteome; Ligase;
 KM Peptidoglycan synthesis.
 SQ SEQUENCE 459 AA; 50137 MW; 083AB3E45C59DC9 CRC64;
 NP_BIND 119 125 ATP (Potential).
 Query Match 10.0%; Score 6; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TDNCERT 9
 DB 403 TDNCERT 408

RESULT 7
 ID Q9C7H2 PRELIMINARY; PRT; 601 AA.
 AC Q9C7H2;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Hypothetical protein F28P5.4 (A1972090/F28P5_4).
 GN Name=F28P5.4;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 Mafti R., Roming C.M., Koo H., Fujii C.Y., Utterback T.R.,
 Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
 Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
 Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
 Davis R.W., Theologis A., Ecker J.R.;
 Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 Chan M.W., Chang C.H., Dale J.M., Hayashizaki Y., Heuan V.W.,
 Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RA EMBL; AC069273; AAG51137.1; -;
 DR EMBL; AF367274; AAK56263.1; -;
 DR EMBL; BT002712; AA011628.1; -;
 DR PIR; B96744; B96744.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0005506; F: iron ion binding; IEA.
 DR InterPro; IPR006638; E1p3/MiAB/MiFB.
 DR InterPro; IPR006466; MiAB-like B.
 DR InterPro; IPR007197; Radical_SAM.
 DR InterPro; IPR002792; TRAM.
 DR InterPro; IPR005839; UPF0004.
 DR Pfam; PF04055; Radical_SAM; 1.
 DR Pfam; PF01938; TRAM; 1.
 DR Pfam; PF00919; UPF0004; 1.
 DR SMART; SM00729; E1p3; 1.
 DR TIGRPFAMs; TIGR01578; MiAB-like-B; 1.
 DR TIGRPFAMs; TIGR00089; UPF0004; 1.

DR PROSITE; PS09262; TRAM; 1.
 DR PROSITE; PS01278; UPF0004; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 601 AA; 65496 MW; AAC13F7BFCB3DA3D CRC64;
 NP_BIND 119 125 ATP (Potential).
 Query Match 10.0%; Score 6; DB 2; Length 601;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CERTCTC 12
 DB 514 CERTCTC 519

RESULT 8
 ID PRTS_SERMA STANDARD; PRT; 1045 AA.
 AC P09489;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Extracellular serine protease precursor (EC 3.4.21.-).
 OS Serratia marcescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Serratia.
 OC NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-35 AND 407-408.
 RC STRAIN=IFO 3046;
 RX MEDLINE=86223815; PubMed=3011754;
 RA Yanagida N., Uozumi T., Beppu T.;
 "Specific excretion of Serratia marcescens protease through the outer
 RT membrane of Escherichia coli.";
 RL J. Bacteriol. 166:937-944(1986).
 RN [2]
 RP PARTIAL SEQUENCE, AND PROCESSING.
 RX MEDLINE=92348352; PubMed=1639760;
 RA Shikata S., Shimada K., Kataoka H., Hornouchi S., Beppu T.;
 "Detection of large COOH-terminal domains processed from the precursor
 RT of Serratia marcescens serine protease in the outer membrane of
 RL Escherichia coli.";
 RL J. Biochem. 111:627-632(1992).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the peptidase S8 family.
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 CC -----
 DR EMBL; M13469; AAA26572.1; -;
 DR PIR; A29840; A29840.
 DR HSSP; Q99405; 1MPN.
 DR MEROPS; S08_094; -;
 DR InterPro; IPR005546; Auto_transbeta.
 DR InterPro; IPR006315; Autocatalytic.
 DR InterPro; IPR000209; Pept_S8_S53.
 DR InterPro; IPR011165; Pept_S8A_autrans.
 DR Pfam; PF03797; Autocatalytic; 1.
 DR Pfam; PF00082; Peptidase S8; 1.
 DR Pfam; PF000164; Autotr_sbt-like; 1.
 DR PRINTS; PR00723; SUBTILISIN.
 DR TIGRPFAMs; TIGR01414; autocatalytic_bar1; 1.
 DR PROSITE; PS00136; SUBTILASE_ASF; FALSE_NEG.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KM Direct protein sequencing; Hydrolase; Serine protease; Signal;
 Zymogen.
 FT SIGNAL 1 27
 CHAIN 28 645 Extracellular serine protease.

FT PROPEP 646 1045
FT ACT_SITE 76 76 Charge relay system (By similarity).
FT ACT_SITE 112 112 Charge relay system (By similarity).
FT ACT_SITE 341 341 Charge relay system (By similarity).
SQ SEQUENCE 1045 AA, 112345 MW, 4924EA50E4FF179C CRC64;
Query Match 10.0%; Score 6; DB 1; Length 1045;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 15 TEMQTD 20
Db 953 TEMQTD 958
RESULT 9
081A76 PRELIMINARY; PRT, 1068 AA.
ID 081A76
AC 081A76;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2004 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform b.
GN Name=P11-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wohldmann P., Beck C.;
RT "The sequence of C. elegans cosmid K10F12.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- STIMULATORY: Contains 1 C2 domain.
DR EMBL; AF025462; AA02423.1; -.
DR HSSP; P10688; IDJH.
DR WormBase; WBGene00004045; p11-1.
DR WormPEP; K10F12.3b; CE31037.
DR GO; GO:0004435; F:phosphoinositide phospholipase C activity; IEA.
DR GO; GO:0006229; P:intracellular signalling cascade; IEA.
DR InterPro; IPR000008; C2.
DR InterPro; IPR008973; C2_CaLB.
DR InterPro; IPR001849; PH.

DR InterPro; IPR011036; PH related.
DR InterPro; IPR001192; PI_PLC.
DR InterPro; IPR000909; PI_PLC_X.
DR InterPro; IPR001711; PI_PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00388; PI_PLC-X; 1.
DR Pfam; PF00387; PI_PLC-Y; 1.
DR PRINTS; PR00360; C2DOMAIN.
DR PRINTS; PR00390; PHPLIPASEC.
DR ProDom; PD001202; PI_PLC_Y; 1.
DR SMART; SM00239; C2; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00148; PLCX; 1.
DR SMART; SM00149; PLCYC; 1.
DR PROSITE; PS50004; C2_DOMAIN_2; 1.
DR PROSITE; PS50007; PI_PLC_X_DOMAIN; 1.
DR PROSITE; PS50008; PI_PLC_Y_DOMAIN; 1.
SQ SEQUENCE 1068 AA, 120042 MW, 9BF7CFCFFD7EC221 CRC64;
Query Match 10.0%; Score 6; DB 2; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 TDNCET 9
Db 310 TDNCET 315
RESULT 10
081A75 PRELIMINARY; PRT, 1075 AA.
ID 081A75
AC 081A75;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Phospholipase C like protein 1, isoform a.
GN Name=P11-1; ORFNames=K10F12.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wohldmann P., Beck C.;
RT "The sequence of C. elegans cosmid K10F12.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;

Query Match 10.0%; Score 6; DB 2; Length 1870;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCERTCT 11
 |||||
 Db 241 NCERTCT 246

RESULT 14
 ID LMA2 HUMAN STANDARD; PRT; 3110 AA.
 AC P24043; Q14736; Q93022;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain).
 GN Name=LMA2; Synonyms=LMM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94124633; PubMed=8294519; DOI=10.1083/jcb.124.3.381;
 RA Vuolteenaho R., Nissinen M., Sainio K., Byers M., Eddy R.,
 RA Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K.;
 RT "Human laminin M chain (merosin): complete primary structure,
 RT chromosomal assignment, and expression of the M and A chain in human
 RT fetal tissues."; Cell Biol. 124:381-394(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97066955; PubMed=8910357; DOI=10.1074/jbc.271.44.27664;
 RA Zhang X., Vuolteenaho R., Tryggvason K.;
 RT "Structure of the human laminin alpha2-chain gene (LMA2), which is
 RT affected in congenital muscular dystrophy."; J. Biol. Chem. 271:27664-27669(1996).
 RN [3]
 RP SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=90238994; PubMed=2185464;
 RA Ehrig K., Leivo I., Argraves W.S., Ruoslahti E., Engvall E.;
 RT "Merosin, a tissue-specific basement membrane protein, is a laminin-
 RT like protein."; Proc. Natl. Acad. Sci. U.S.A. 87:3264-3268(1990).
 RN [4]
 RP VARIANTS GLN-545; HIS-619; LEU-919; HIS-2586 AND LYS-2614.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluft G.A., Amato A.A., Mendell J.R.;
 RT "Novel single base polymorphisms and rare sequence variants in the
 RT laminin 2-chain coding region detected by RNA/SSCP analysis."; Hum. Mutat. 13:174-174(1999).
 RN [5]
 RP ERKATM.
 RA Panicker S.G., Mendell J.T., Chen L., Feng B., Sahenk Z.,
 RA Marzluft G.A., Amato A.A., Mendell J.R.;
 RT Hum. Mutat. 13:340-340(1999).
 RN [6]
 RP VARIANT MDCL1 PRO-2564.
 RX MEDLINE=21476011; PubMed=11591858;
 RA He Y., Jones K.J., Vignier N., Morgan G., Chevallay M., Barois A.,
 RA Besoune-Machlud B., Hori H., Mizuta T., Tome F.M.S., North K.N.,
 RA Guicheney P.;
 RT "Congenital muscular dystrophy with primary partial laminin alpha-2
 RT chain deficiency: molecular study."; Neurology 57:1319-1322(2001).
 RN [7]
 RP VARIANTS MDCL1 TYR-527 AND ARG-862.
 RX MEDLINE=22439669; PubMed=12552555; DOI=10.1002/humu.10157;

RA Tezak Z., Prandini P., Boscaro M., Marin A., Devaney J., Marino M.,
 RA Fatin M., Trevisan C.P., Park J., Tyson W., Finkel R., Garcia C.,
 RA Angelini C., Hoffman E.P., Pegoraro E.;
 RT "Clinical and molecular study in congenital muscular dystrophy with
 RT partial laminin alpha-2 (LMA2) deficiency."; Hum. Mutat. 21:103-111(2003).
 RL Hum. Mutat. 21:103-111(2003).
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
 CC is thought to mediate the attachment, migration and organization
 CC of cells into tissues during embryonic development by interacting
 CC with other extracellular matrix components.
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
 CC different polypeptide chains (alpha, beta, gamma), which are bound
 CC to each other by disulfide bonds into a cross-shaped molecule
 CC comprising one long and three short arms with globules at each
 CC end. The alpha-2 chain is a subunit of laminin-2 (merosin) and
 CC laminin-4 (S-merosin).
 CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
 CC membranes (major component).
 CC -1- TISSUE SPECIFICITY: Placenta, striated muscle, peripheral nerve,
 CC cardiac muscle, pancreas, lung, spleen, kidney, adrenal gland,
 CC skin, testis, meninges, choroid plexus, and some other regions of
 CC the brain; not in liver, thymus and bone.
 CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
 CC with other laminin chains to form a coiled coil structure.
 CC -1- DOMAIN: Domains VI, IV and G are globular.
 CC -1- DISEASE: Defects in LMA2 are the cause of merosin-deficient
 CC congenital muscular dystrophy type 1A (MDCL1) [MIM:607855]. MDCL1
 CC is characterized by difficulty walking, hypotonia, proximal
 CC weakness, hyporeflexia, and white matter hypodensity on MRI.
 CC -1- SIMILARITY: Contains 1 laminin EGF-like domains.
 CC -1- SIMILARITY: Contains 5 laminin G-like domains.
 CC -1- SIMILARITY: Contains 2 laminin IV domains.
 CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z26653; CAAB1394.1; -;
 DR EMBL; U66796; AAB18388.1; JOINED.
 DR EMBL; U66733; AAB18388.1; JOINED.
 DR EMBL; U66734; AAB18388.1; JOINED.
 DR EMBL; U66735; AAB18388.1; JOINED.
 DR EMBL; U66736; AAB18388.1; JOINED.
 DR EMBL; U66737; AAB18388.1; JOINED.
 DR EMBL; U66738; AAB18388.1; JOINED.
 DR EMBL; U66739; AAB18388.1; JOINED.
 DR EMBL; U66740; AAB18388.1; JOINED.
 DR EMBL; U66741; AAB18388.1; JOINED.
 DR EMBL; U66742; AAB18388.1; JOINED.
 DR EMBL; U66743; AAB18388.1; JOINED.
 DR EMBL; U66745; AAB18388.1; JOINED.
 DR EMBL; U66746; AAB18388.1; JOINED.
 DR EMBL; U66747; AAB18388.1; JOINED.
 DR EMBL; U66748; AAB18388.1; JOINED.
 DR EMBL; U66749; AAB18388.1; JOINED.
 DR EMBL; U66750; AAB18388.1; JOINED.
 DR EMBL; U66751; AAB18388.1; JOINED.
 DR EMBL; U66752; AAB18388.1; JOINED.
 DR EMBL; U66753; AAB18388.1; JOINED.
 DR EMBL; U66754; AAB18388.1; JOINED.
 DR EMBL; U66755; AAB18388.1; JOINED.
 DR EMBL; U66756; AAB18388.1; JOINED.
 DR EMBL; U66757; AAB18388.1; JOINED.
 DR EMBL; U66758; AAB18388.1; JOINED.
 DR EMBL; U66759; AAB18388.1; JOINED.
 DR EMBL; U66760; AAB18388.1; JOINED.
 DR EMBL; U66761; AAB18388.1; JOINED.
 DR EMBL; U66762; AAB18388.1; JOINED.

DR EMBL; U66763; AAB18388.1; JOINED.
DR EMBL; U66764; AAB18388.1; JOINED.
DR EMBL; U66765; AAB18388.1; JOINED.
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DR EMBL; U66768; AAB18388.1; JOINED.
DR EMBL; U66769; AAB18388.1; JOINED.
DR EMBL; U66770; AAB18388.1; JOINED.
DR EMBL; U66771; AAB18388.1; JOINED.
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DR EMBL; U66778; AAB18388.1; JOINED.
DR EMBL; U66779; AAB18388.1; JOINED.
DR EMBL; U66780; AAB18388.1; JOINED.
DR EMBL; U66781; AAB18388.1; JOINED.
DR EMBL; U66782; AAB18388.1; JOINED.
DR EMBL; U66783; AAB18388.1; JOINED.
DR EMBL; U66784; AAB18388.1; JOINED.
DR EMBL; U66785; AAB18388.1; JOINED.
DR EMBL; U66786; AAB18388.1; JOINED.
DR EMBL; U66787; AAB18388.1; JOINED.
DR EMBL; U66788; AAB18388.1; JOINED.
DR EMBL; U66789; AAB18388.1; JOINED.
DR EMBL; U66790; AAB18388.1; JOINED.
DR EMBL; U66791; AAB18388.1; JOINED.
DR EMBL; U66792; AAB18388.1; JOINED.
DR EMBL; U66793; AAB18388.1; JOINED.
DR EMBL; U66794; AAB18388.1; JOINED.
DR EMBL; U66795; AAB18388.1; JOINED.
DR EMBL; M59832; AAA63215.1; -.
DR PIR; PX0082; MMHUM.
DR HSSP; Q60675; 1DYK.
DR Genew; HGNC:6482; LAMN2.
DR MIM; 156225; -.
DR MIM; 607855; -.
DR GO; GO:0005604; C:basement membrane; TAS.
DR GO; GO:0005198; F:structural molecule activity; TAS.
DR GO; GO:0007517; P:muscle development; TAS.
DR InterPro; IPR008985; Com_1like_1ec_91.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008979; Gal_bind_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR009254; Laminin_I.
DR InterPro; IPR010307; Laminin_II.
DR InterPro; IPR008211; Laminin_N.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00052; Laminin_B_2.
DR Pfam; PF00053; Laminin_EGF; 14.
DR Pfam; PF00054; Laminin_G; 5.
DR Pfam; PF06008; Laminin_I; 1.
DR Pfam; PF06009; Laminin_II; 1.
DR Pfam; PF00055; Laminin_N; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR ProDom; PD003031; Laminin_B; 2.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50025; LAM_G_DOMAIN; 5.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 14.
KW Basement membrane; Cell adhesion; Coiled coil;
KW Congenital muscular dystrophy; Direct protein sequencing;

Query Match 10.0%; Score 6; DB 1; Length 3110;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 NCETCT 11
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DB 389 NCETCT 394
RESULT 15
DEF4_ANDAU STANDARD; PRT; 37 AA.
AC P56686; P81618;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 4 kDa defensin.
OS Androctonus australis (Sahara scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butridae; Butthoidea; Butthidae; Androctonus.
OX NCBI_TaxId=6858;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC STRAIN=Hector; TISSUE=Hemolymph;
RX MEDLINE=97094646; PubMed=8939880; DOI=10.1074/jbc.271.47.29537;
RA Bhret-Sabatier L., Loew D., Goyffon M., Fehlbauer P., Hoffmann J.A.,
RA van Dorsselaer A., Bulot P.
RT "Characterization of novel cysteine-rich antimicrobial peptides from
RT scorpion blood.";
RL J. Biol. Chem. 271:29537-29544(1996).
CC -1- FUNCTION: Active against Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=4206.8; METHOD=Electrospray; RANGE=1-37;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the arthropod defensin family. Subfamily 2.
DR HSSP; P80571; IFUN.
DR InterPro; IPR001542; Defensin_2.
DR Pfam; PF01097; Defensin_2; 1.
DR PROSITE; PS00425; ARTHROPOD_DEFENSINS; 1.
KW Antibiotic; Defensin; Direct protein sequencing.
FT DISULFID 4 25 By similarity.
FT DISULFID 11 33 By similarity.
FT DISULFID 15 35 By similarity.
SQ SEQUENCE 37 AA; 4212 MW; AB1363EC53FB84C1 CRC64;

Query Match 8.3%; Score 5; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 4, 2005, 14:33:22
Job time : 103.982 secs

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